

#6

Figure 1

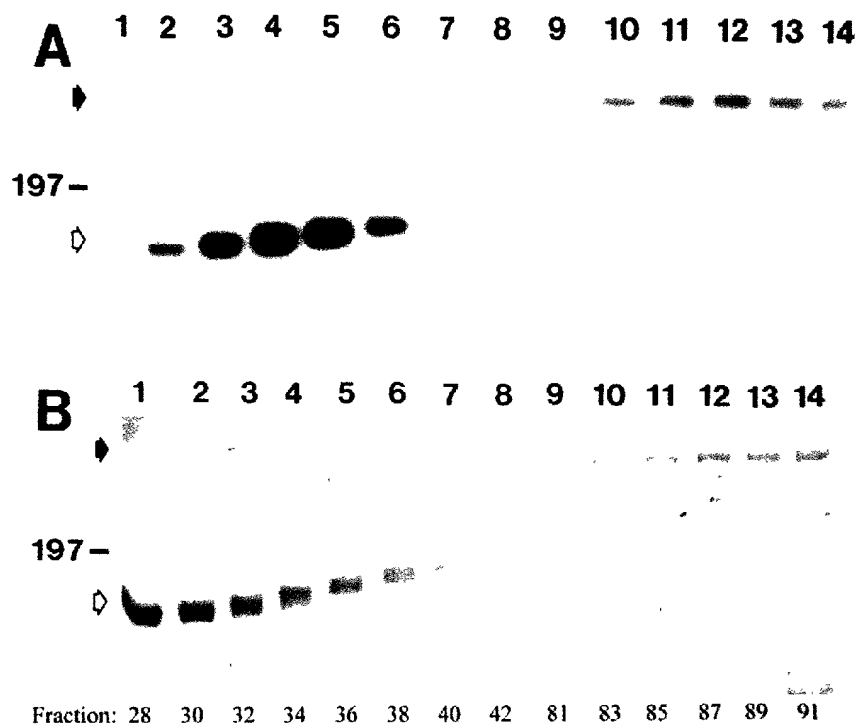


Figure 2

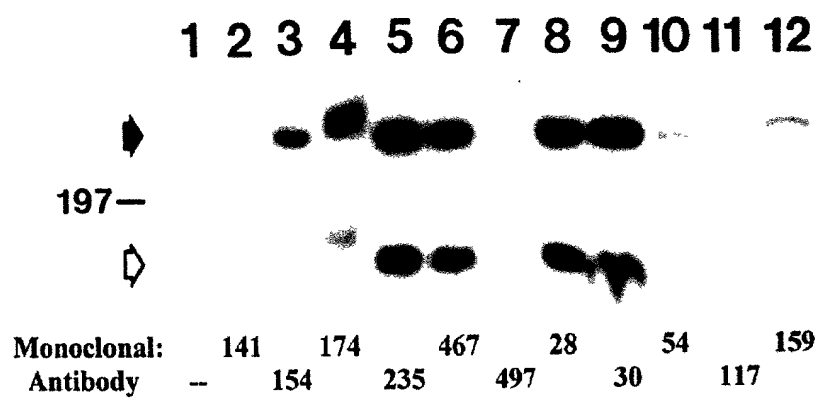


Figure 3

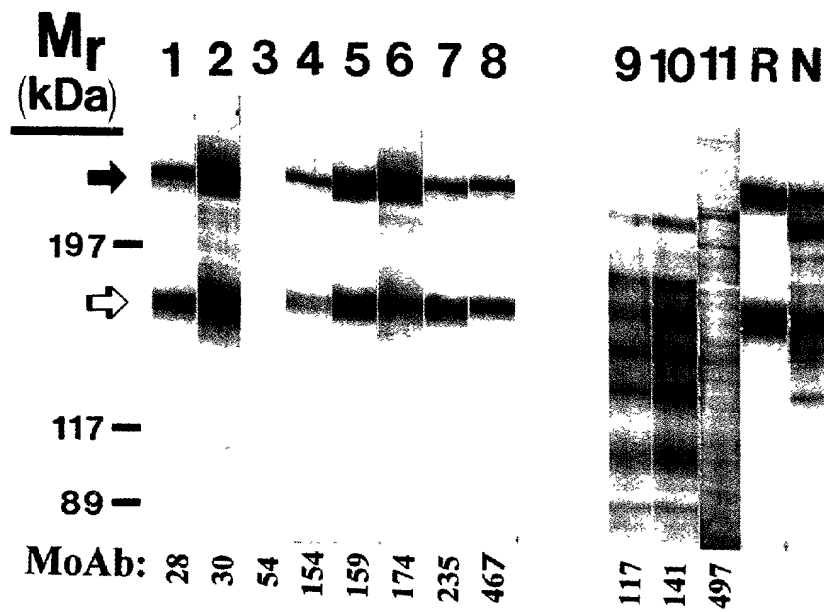


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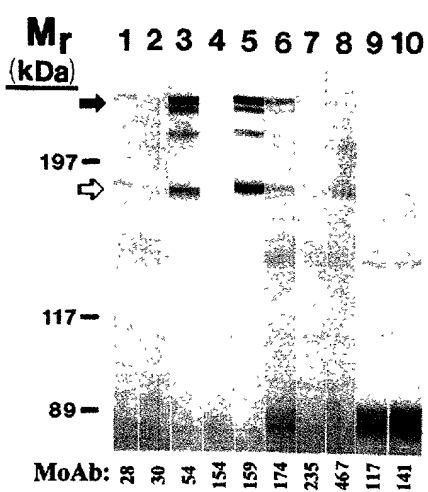


Figure 5

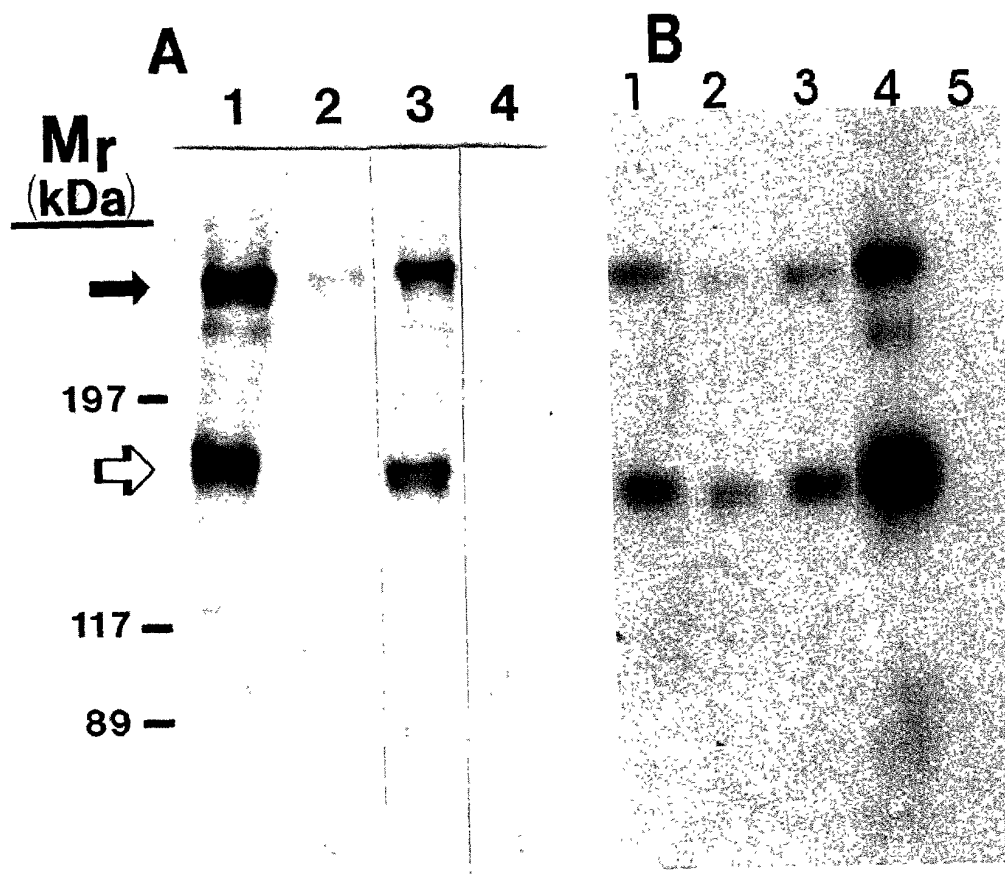


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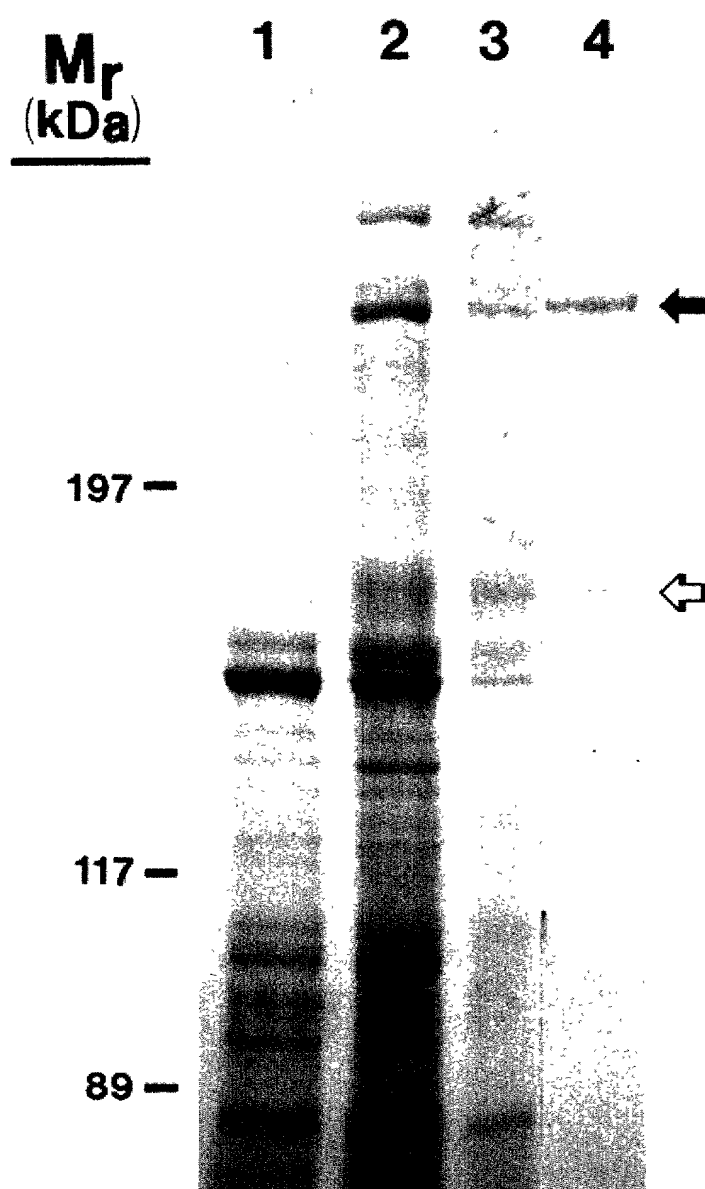


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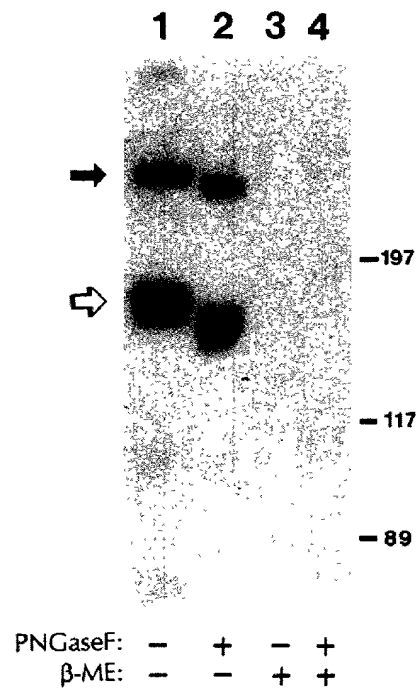
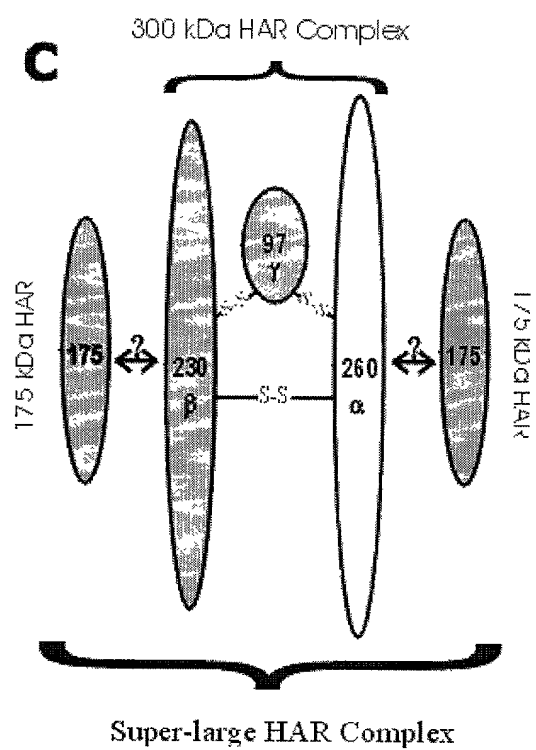
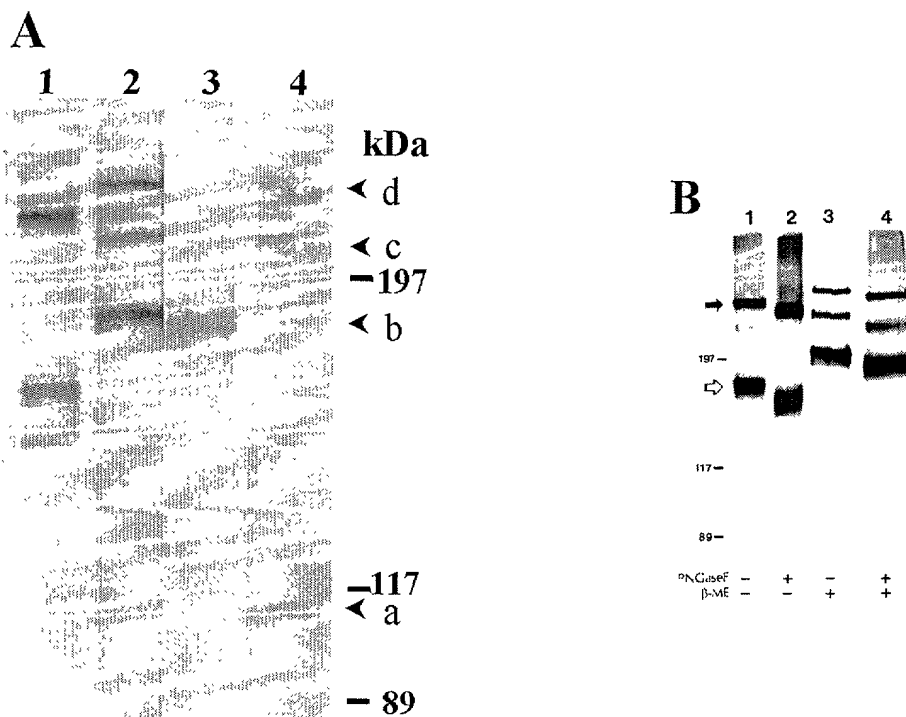


Figure 8



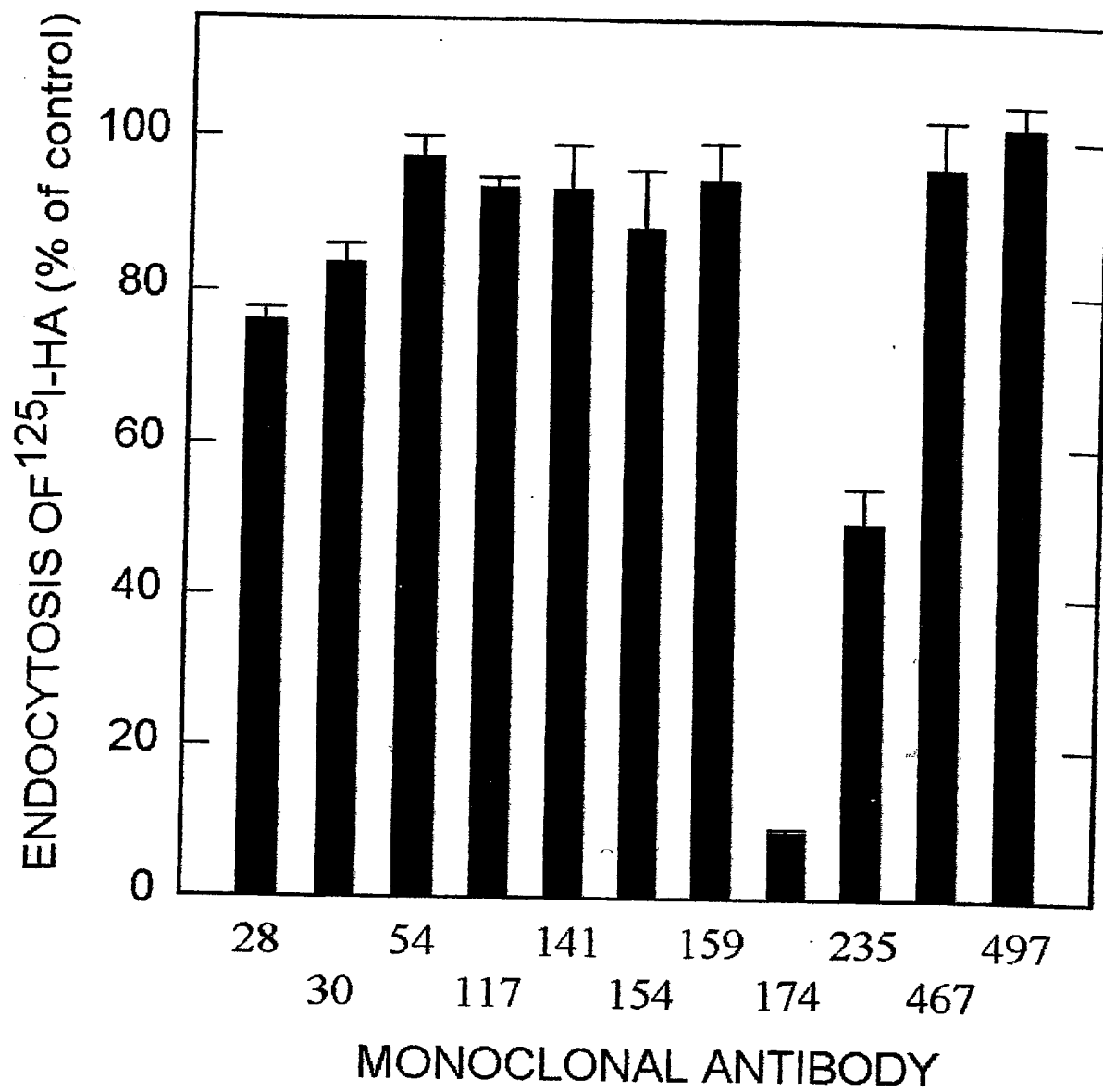


Figure 9

Figure 10

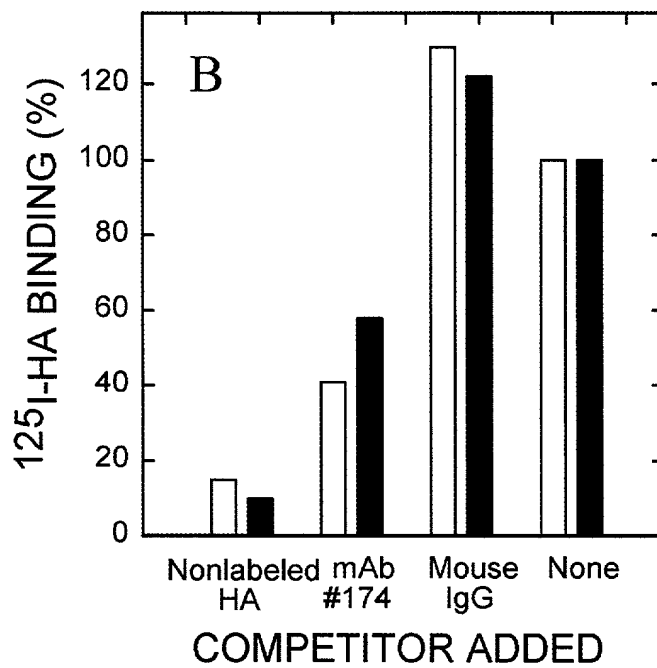
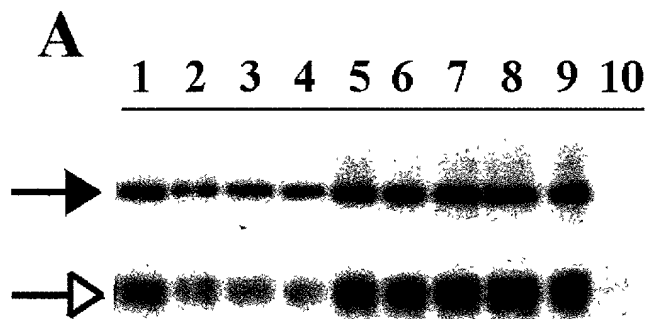


Figure 11

Antibody Inhibition of HA Endocytosis by HARE in LECs

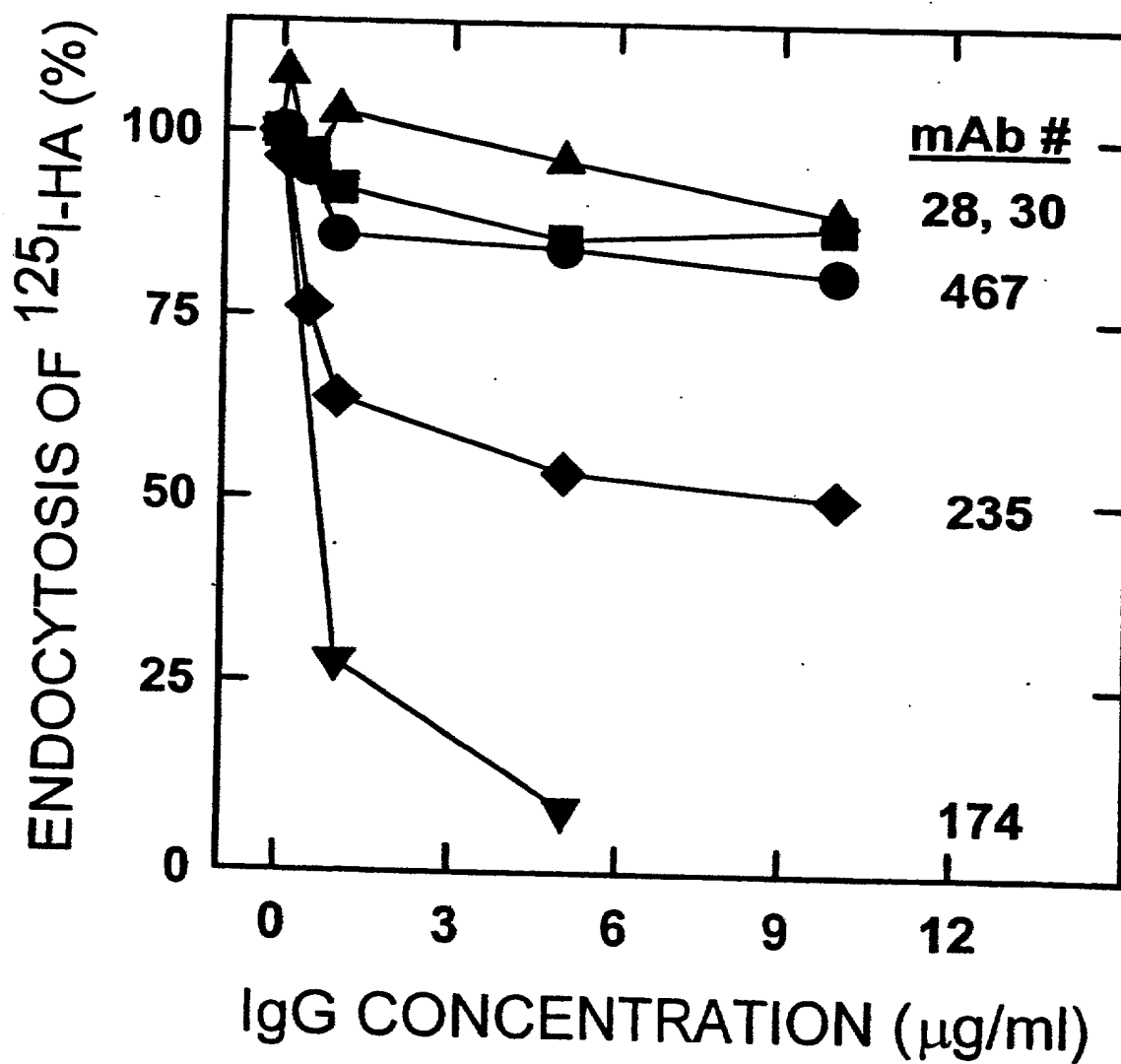


Figure 12

**Antibody Inhibition of HA Binding to HARE
on LECs is Temperature Dependent**

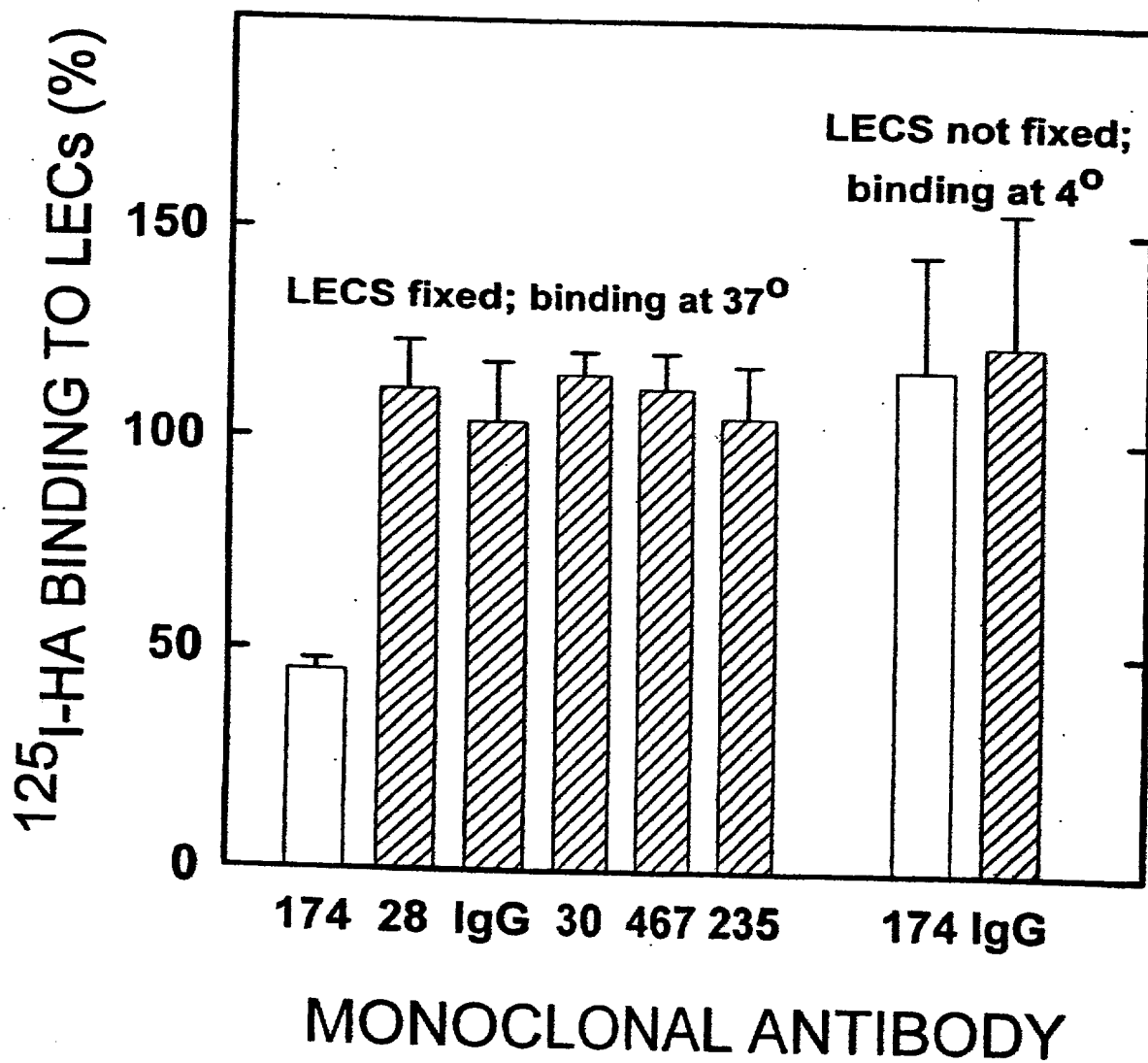


Figure 13

Figure 13

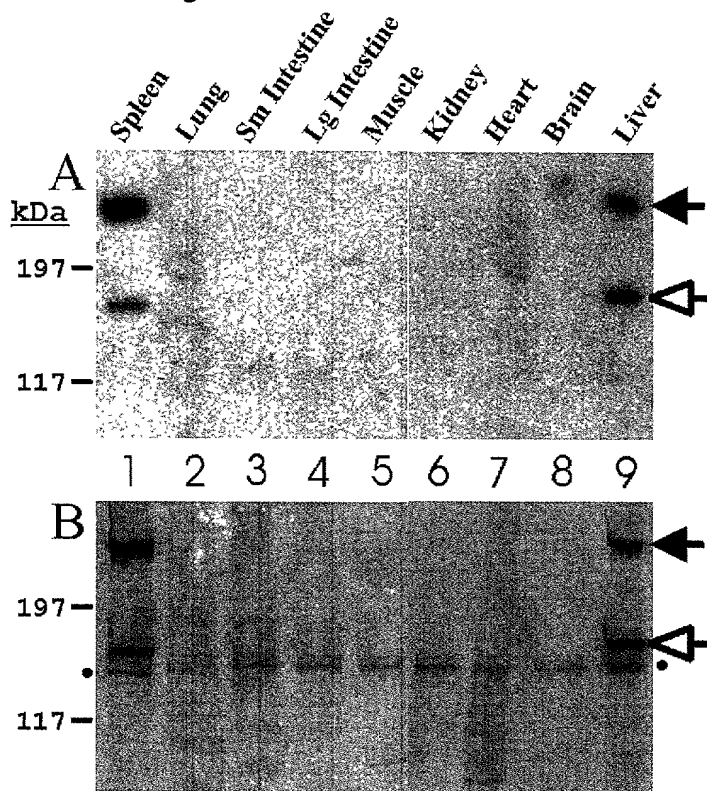
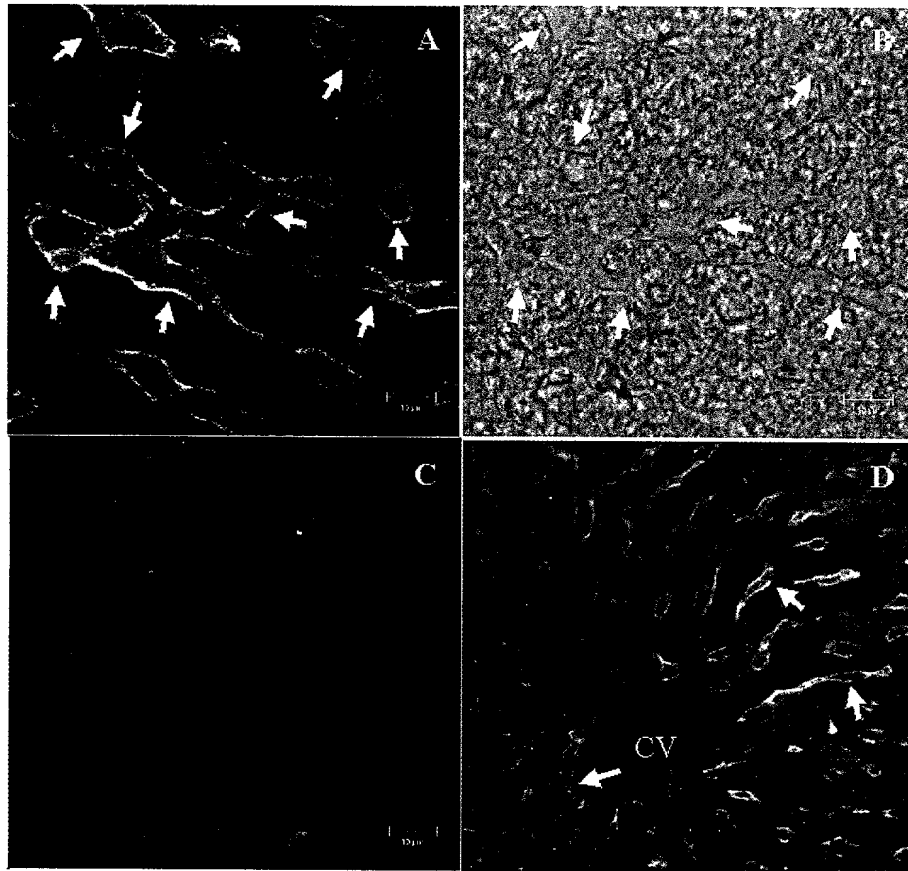


Figure 14



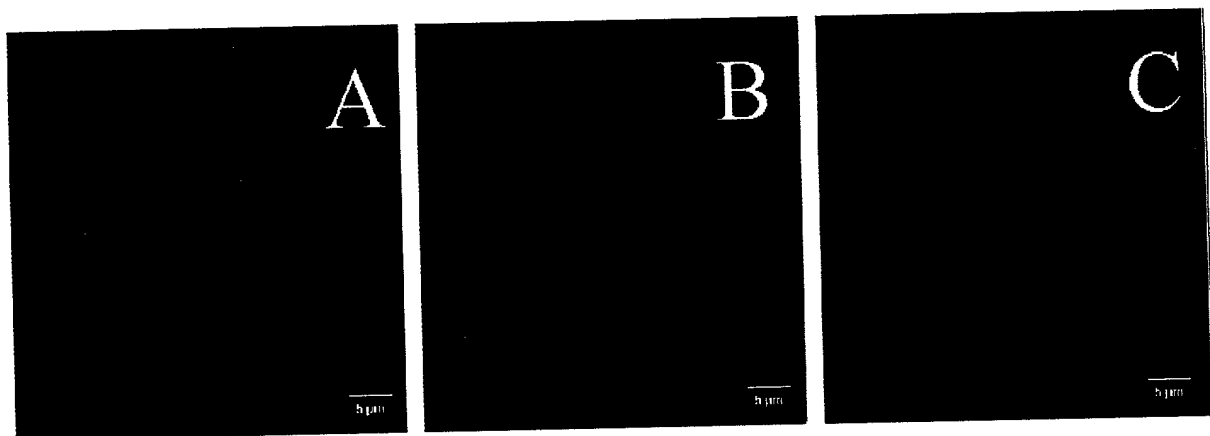
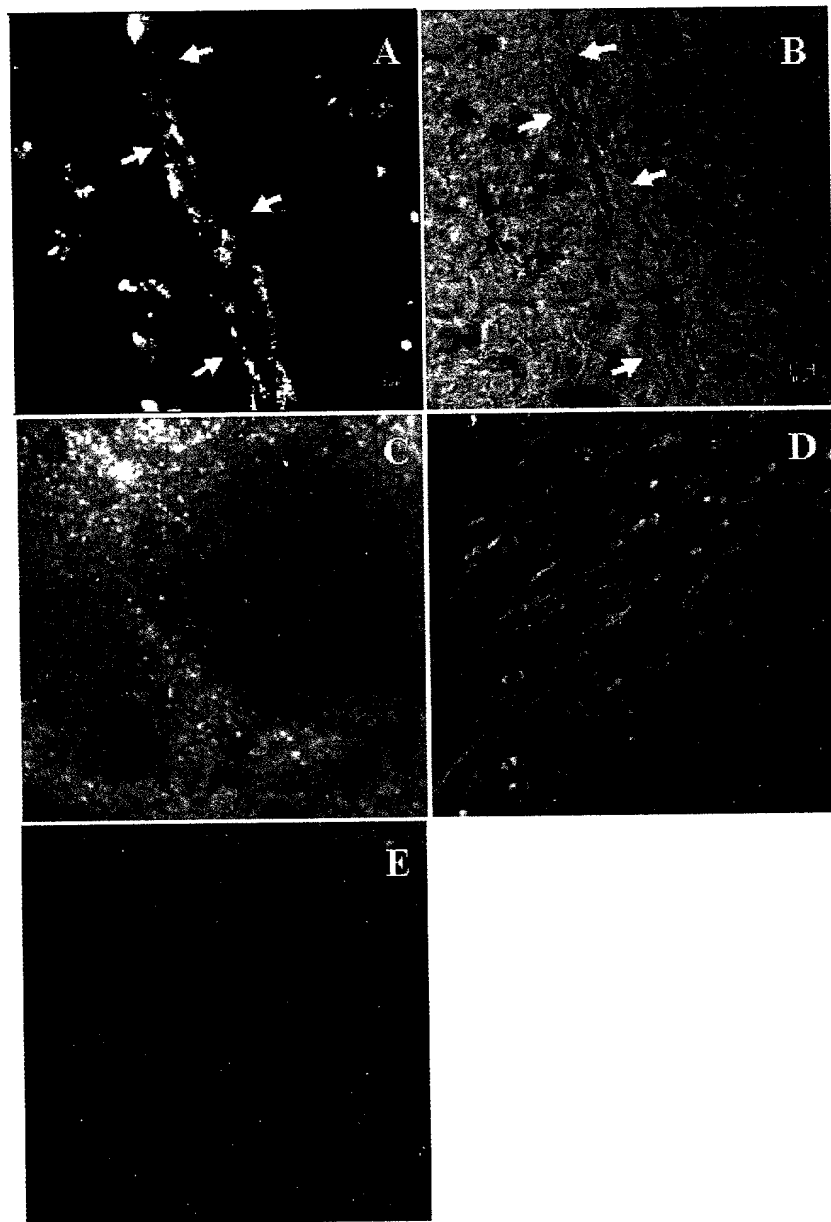


Figure 15

Figure 16



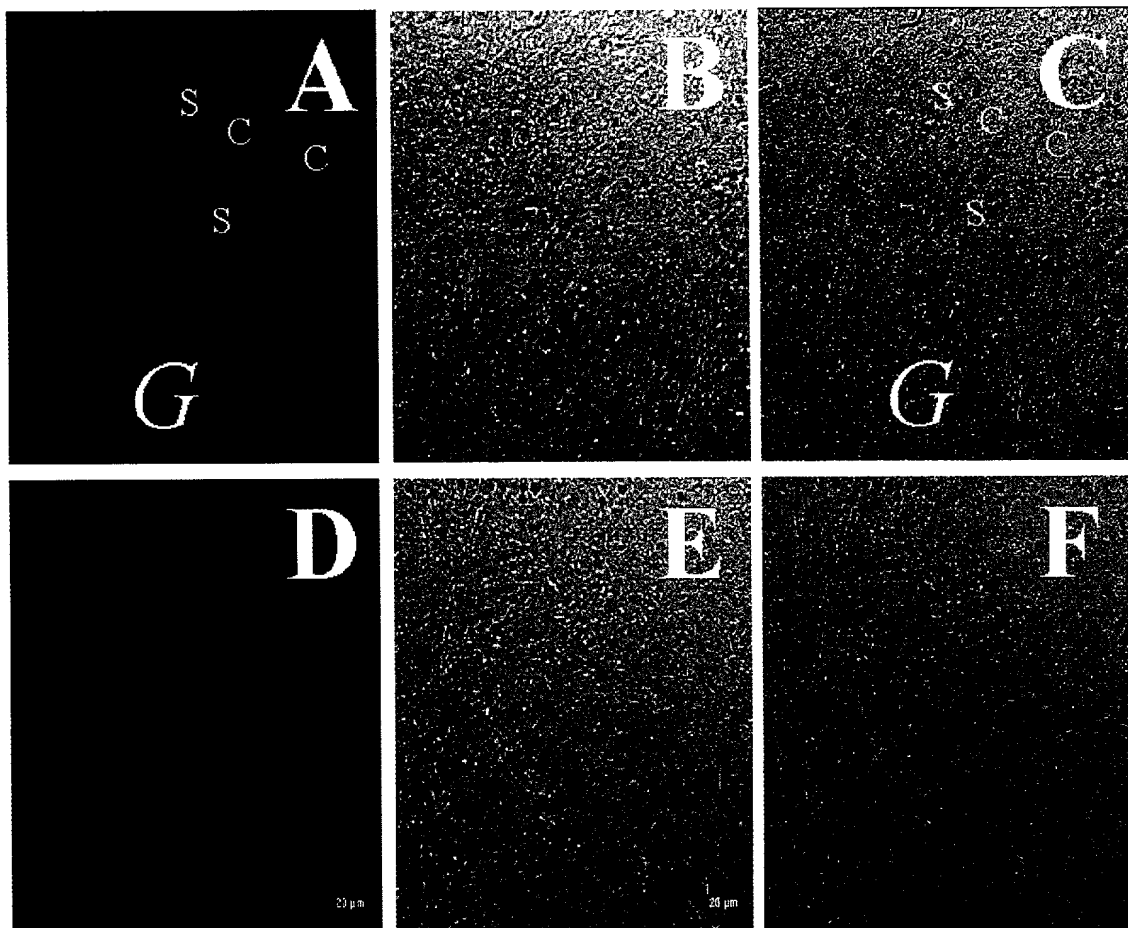
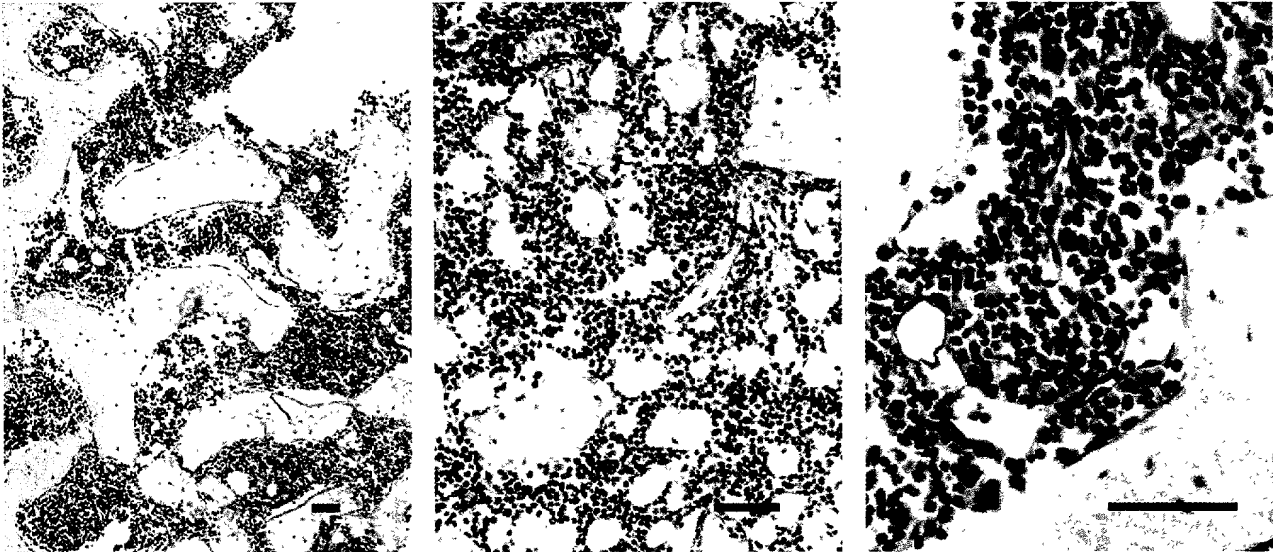


Figure 17

Figure 18

**Immunolocalization of HARE
in Bone Marrow**

Control



Bars = 50 um

Figure 19

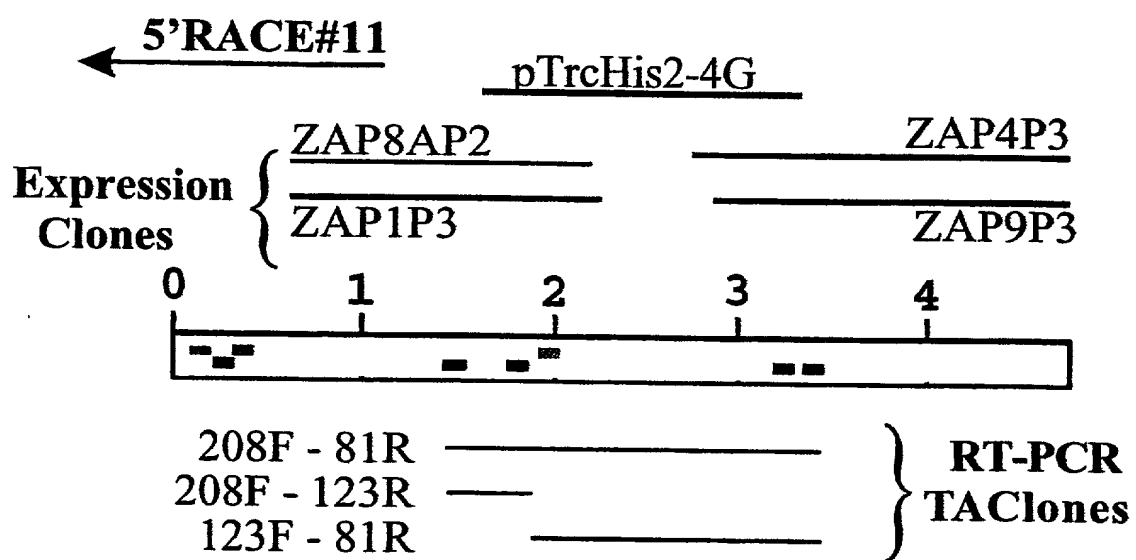


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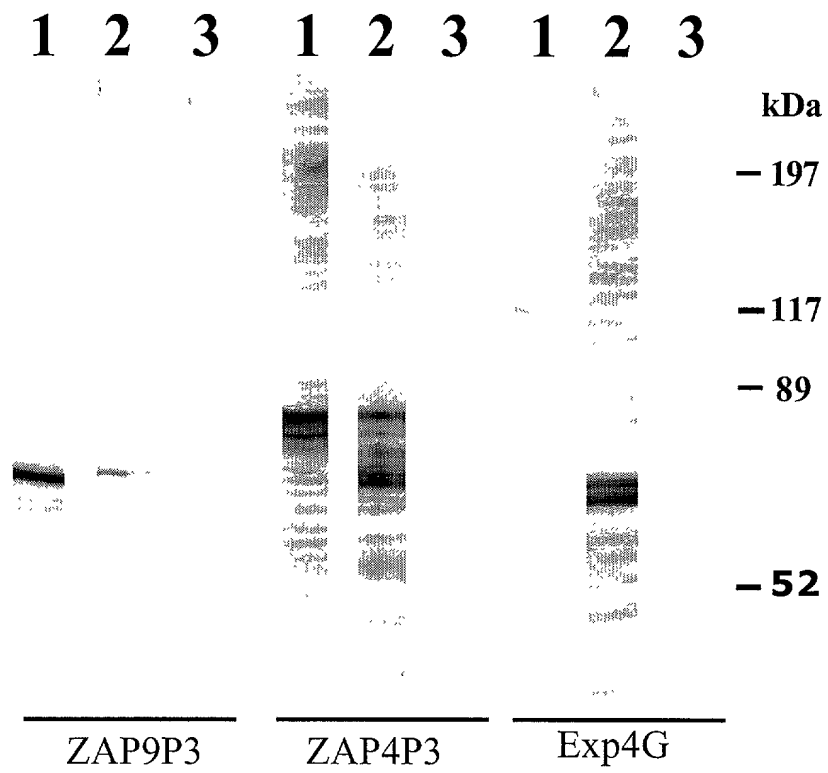


Figure 21

[illegible]

Figure 22

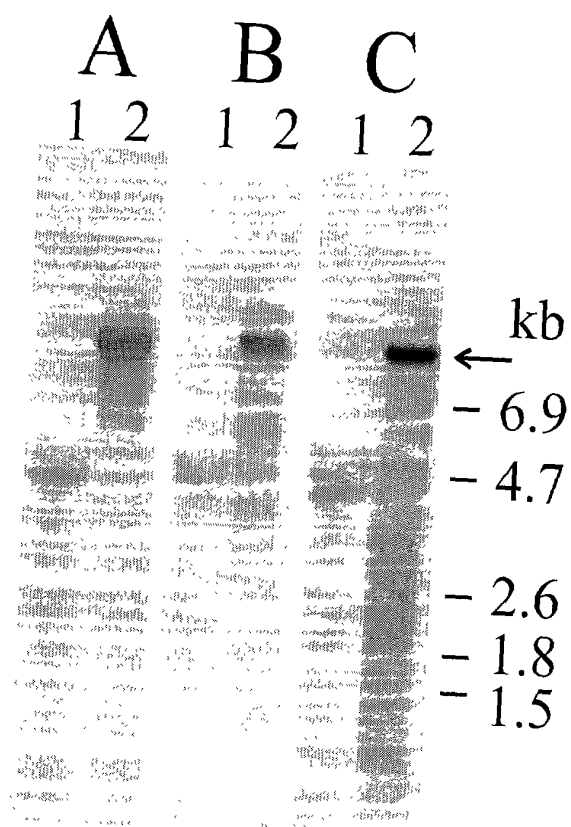


Figure 25

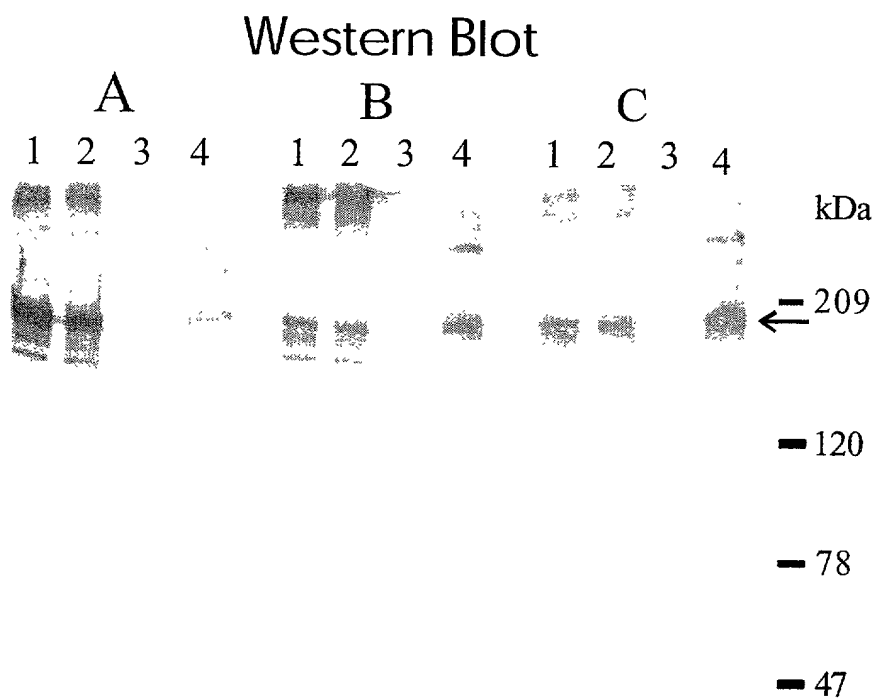
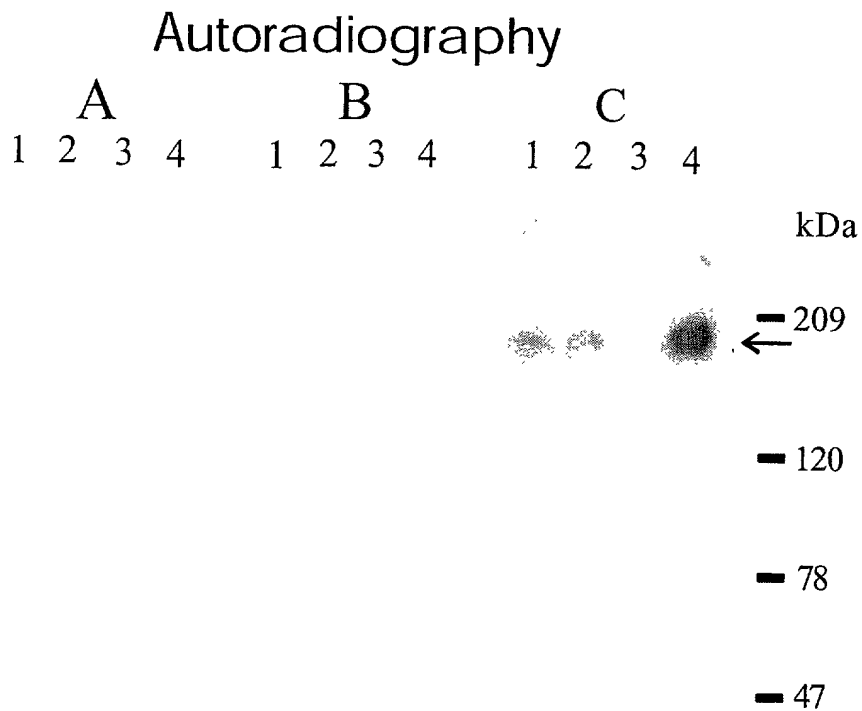


Figure 26

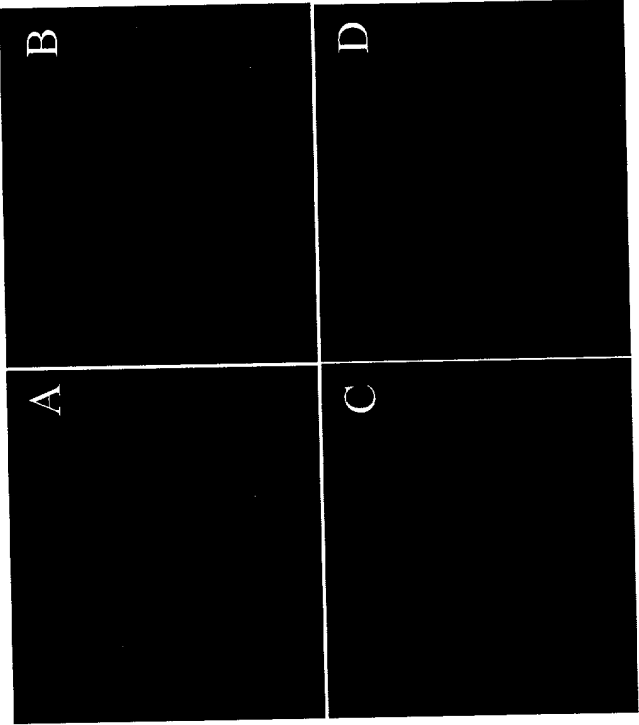


Figure 27A

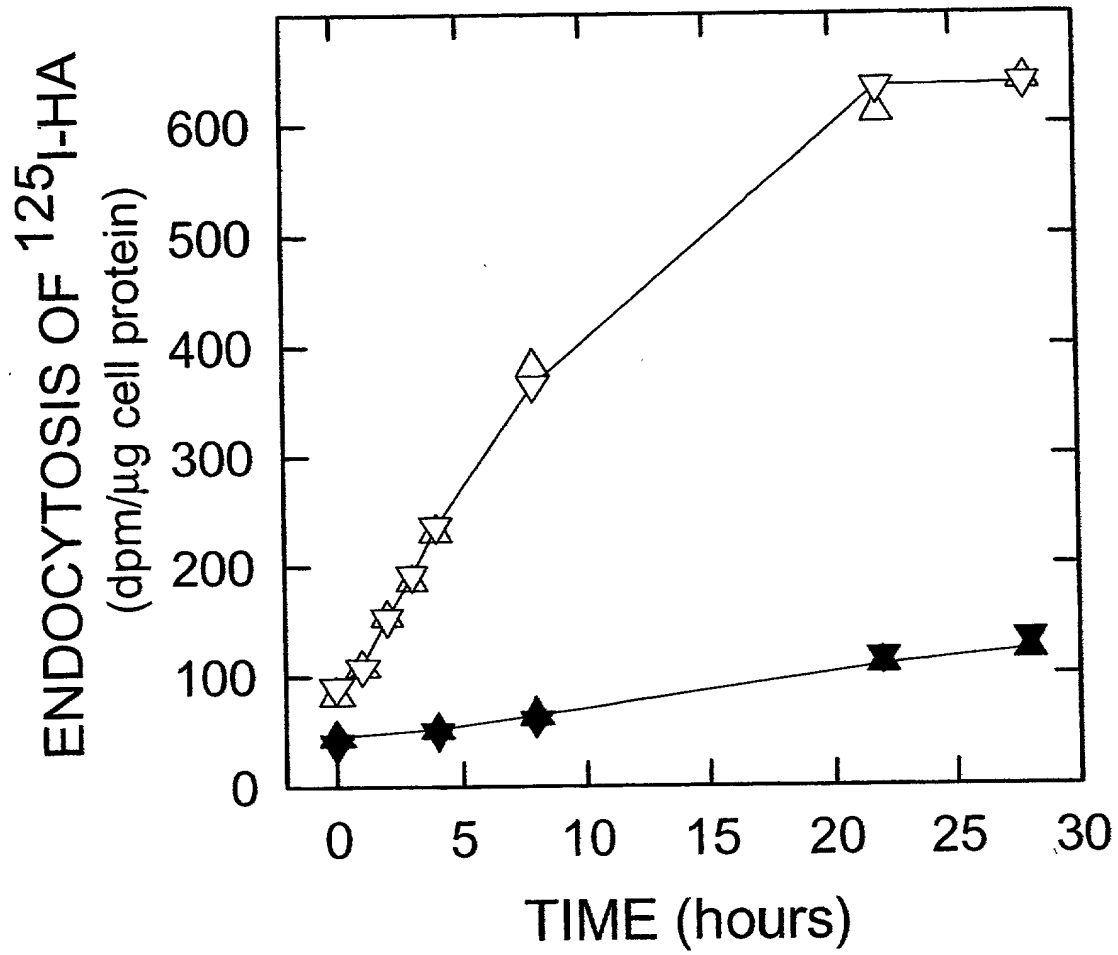


Figure 27B

Degradation of internalized HA by transfected SK-Hep1 cell lines expressing the 175-kDa HARE

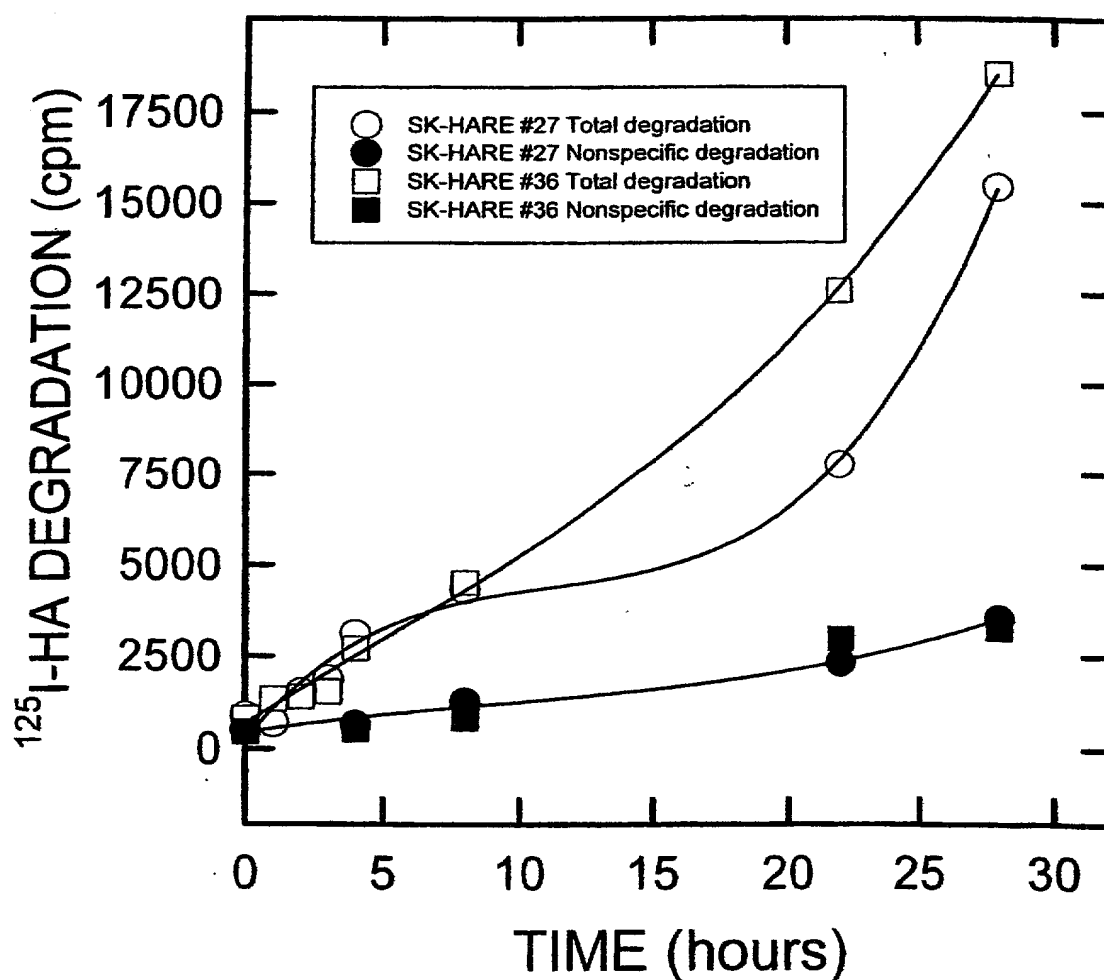


Figure 27C

Hyperosmolarity inhibits HA endocytosis mediated by HARE in transfected SK-Hep1 cells

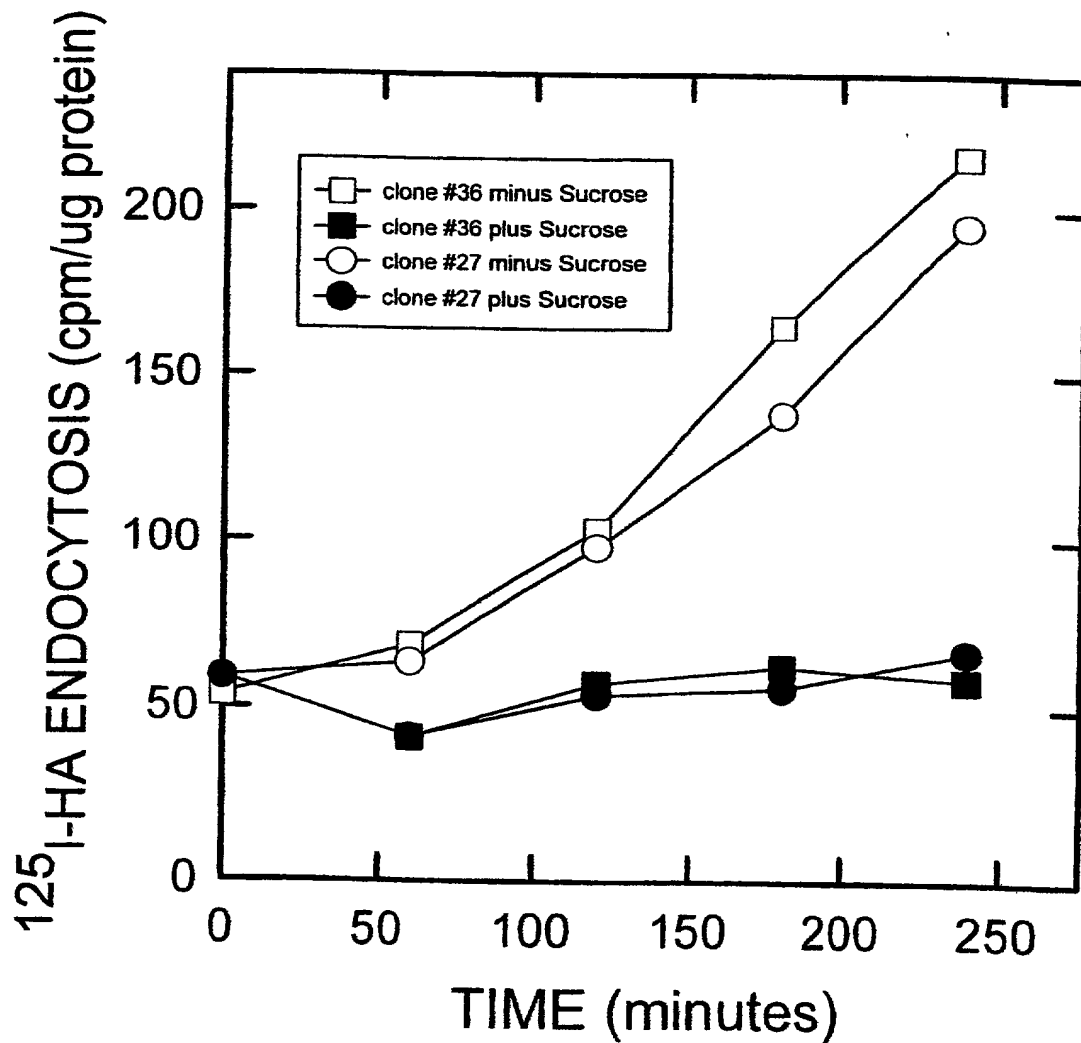


Figure 27D

**Specific monoclonal antibodies against HARE
inhibit HA endocytosis in SK-Hep1
transfectants expressing the 175-kDa HARE**

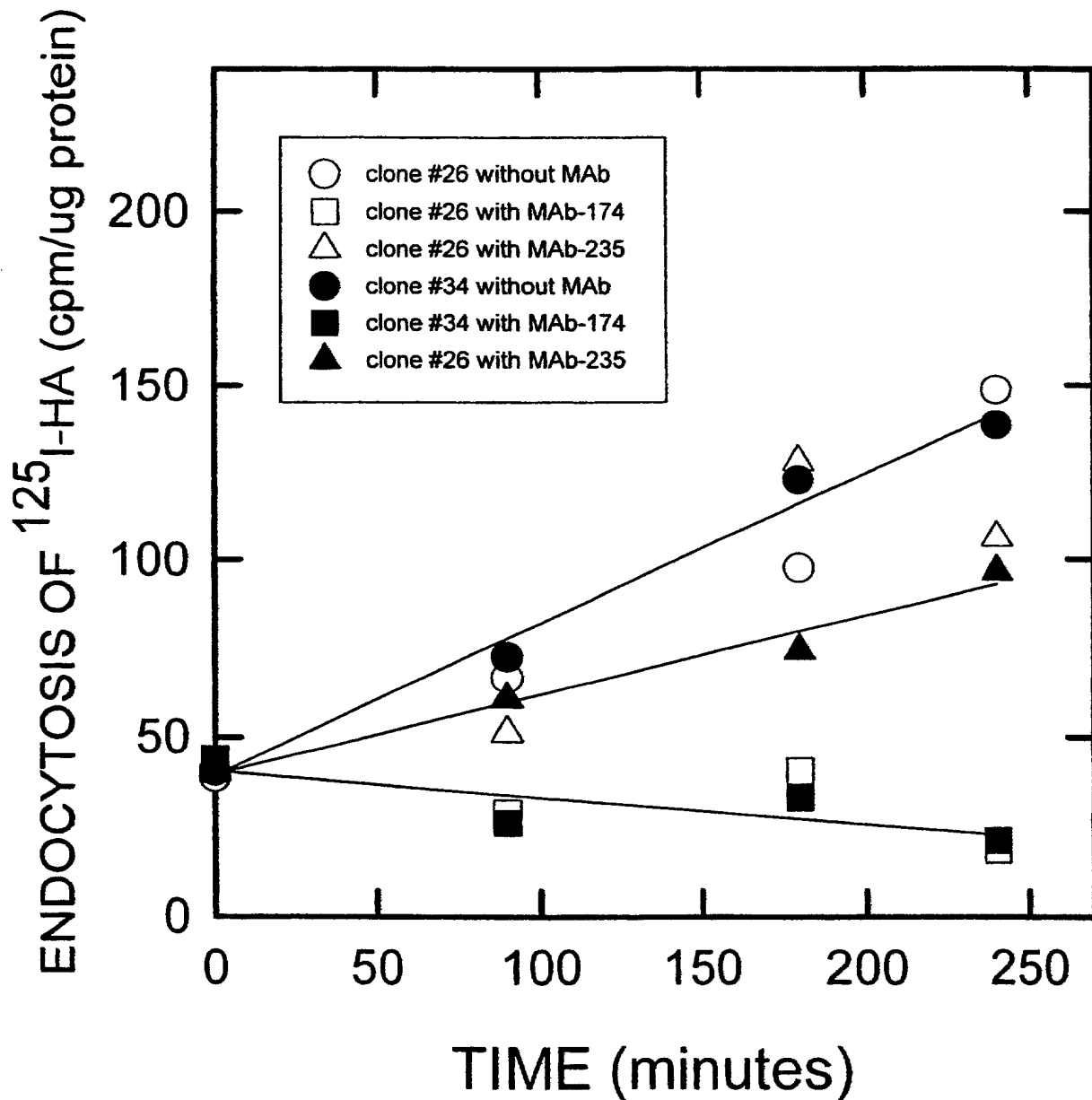


Figure 28

175SHARE 1 ----- SLFS LLTRLBQMPD YSIPRGYIHH YNLASIAESA DAYTVFVPPN EAIENYIREK KATSLKEDIL RYHVVLGELK LKNDLHNGMH REIMLGPSYL
CAB61827 1111 LHILSQVLLP PRGDVPGQCG LLQQLDLVPA FSLPRELLQH HGUVQPIEAA TAYTIFVPTN RSLA---QG NSSHLADATV RHHVVLGEAL SMETLRKGGH RNSLLGPAHW
BAA13377 754 LHILSQVLLP PRGDVPGQCG LLQQLDLV-A FSLPRELLQH HGUVQPIEAA TAYTIFVPTN RSLA---QG NSSHLADATV RHHVVLGEAL SMETLRKGGH RNSLLGPAHW

175SHARE 95 LAFPLRNQQL YVNEAPINVT NVATDKGVH GLEKVLBIQK NRNNNDTII VGRHSGKSO QAPPLETKP LRETRK-IV SIYPMGKRSV FICQPCQVR TITRAVLA
CAB61827 1218 IVFVNHSSQP EVNHVPLBGP MLEAPGRSLI GLSGVLTVGS SRLLHSHAEA LREKVVNTR RFRITQGFOL QDTPRKSIV RSGGFSFR-- --G-SYTLAK KIQVPLCPG
BAA13377 861 IVFVNHSSQP EVNHVPLBGP MLEAPGRSLI GLSGVLTVGS SRLLHSHAEA LREKVVNTR RFRITQGFOL QDTPRKSIV RSGGFSFR-- --G-SYTLAK KIQVPLCPG

175SHARE 204 SLAHNAKPAF GEVKN-MALG TASVMDGVNG TGT-GLGLGF NGTANETTE GKYGIIHQDA SSTVHGRNQ GPLADGSDI DUGWRGVKID MEITTDNNG THTSANTLL
BAB15793 1 -----W HLFQWS--DG TGVLEBEGF SSTANETTE GKYGIIHQDA SSTVHGRNQ GPLADGSDI DUGWRGVKID NATTEDNNG THTSANTLL
CAB61358 1 -----VG
CAB61827 1224 FFGTLCPCP GGLGGV-S-G HGQCCQRFLG SGEH-HEGF HGTANBVEL GRGYNTTGV DPAHGLQOE GLQDGSIV NVGWOGLRD QKITSQPFR KIDNANVQ
BAA13377 967 FFGTLCPCP GGLGGV-S-G HGQCCQRFLG SGEH-HEGF HGTANBVEL GRGYNTTGV DPAHGLQOE GLQDGSIV NVGWOGLRD QKITSQPFR KIDNANVQ

175SHARE 313 DPGDKASIK AAGFPNGTV TAINAETS NGG-STKAL KRTTPGNRV VKRAGYTGID IVLEINPL ENHGGDRNA BTQTGNQA VNLPLKYTG DG-KVSLIN
BAB15793 90 NSDQASIK AAGFCNGTV TAINAETS NGG-SAKAL KRTTPGNRV VKRAGYTGID IVLEINPL ENHGGDRNA BTQTGNQA ANLPLAYTG DG-KVTLIN
CAB61358 3 EAVGTASIK AAGFCNGTV TAINAETS NGG-SAKAL KRTTPGNRV VKRAGYTGID IVLEINPL ENHGGDRNA BTQTGNQA ANLPLAYTG DG-KVTLIN
CAB61827 1433 DSAGASTIA AAGYSNGNIF SEVDPAHG HGG-SPHAN TKVAPQRTI TQDGYMGD ELQEINSL IHGGGHIHA BTPTGQQV SLSREGYS DGIRTLLD
BAA13377 1076 DSAGASTIA AAGYSNGNIF SEVDPAHG HGG-SPHAN TKVAPQRTI TQDGYMGD ELQEINSL IHGGGHIHA BTPTGQQV SLSREGYS DGIRTLLD

175SHARE 422 VLTNNGGS PFAPNTEYQ DQRIK-KPD Y-TGDGIVR GSIYGLPKN PSTSQYFFQL QEHAVRELAG PGPTVFAP-- --LSSSPNHE PRKIDMQQG LMSQVRYHV
BAB15793 199 VLTNNGGS EFAPNHTQO VERTIKKPN Y-TGDGIVR GSIYGLPKN PSTSQYFFQL QEHAVRELAG PGPTVFAP-- --LSSSPNHE PRKIDMQQG LMSQVRYHV
CAB61358 112 VLTNNGGS EFAPNHTQO VERTIKKPN Y-TGDGIVR GSIYGLPKN PSTSQYFFQL QEHAVRELAG PGPTVFAP-- --LSSSPNHE PRKIDMQQG LMSQVRYHV
AAF82398 1 -----MQVLYRYHV
CAB61827 1543 SKNNGGS PYATKSTGD QRTIKKDTA HTVGDGIVR ARVGLLIRD KHAS--FFSL RLLEYKELG DGPTTFVPH ADLMSNLSD ELARIAHRQ L--VFRYHV
BAA13377 1186 SKNNGGS PYATKSTGD QRTIKKDTA HTVGDGIVR ARVGLLIRD KHAS--FFSL RLLEYKELG DGPTTFVPH ADLMSNLSD ELARIAHRQ L--VFRYHV

175SHARE 528 VGLQLLND LKVTTSATLL QGEPVSISSV QDTVDINBA KVLSSDIIST NGVHVIDKL LSPKNLLITP KDALGRVLQN LTTVAANHGY TKFSKLQDS GLLSVITDSI
BAB15793 305 VAHQLLLEN LKLSNATSL QGEPVSISSV QSTVYDNKA KI ISSDIIST NGVHVIDKL LSPKNLLITP KINSGRILQN LTTLATNNGY IKFNSLIQDS GLLSVITDSI
CAB61358 218 VAHQLLLEN LKLSNATSL QGEPVSISSV QSTVYDNKA KI ISSDIIST NGVHVIDKL LSPKNLLITP KINSGRILQN LTTLATNNGY IKFNSLIQDS GLLSVITDSI
AAF82398 10 VAHQLLLEN LKLSNATSL QGEPVSISSV QSTVYDNKA KI ISSDIIST NGVHVIDKL LSPKNLLITP KINSGRILQN LTTLATNNGY IKFNSLIQDS GLLSVITDSI
CAB61827 1649 VGLRLRSED LLEQYATALL SGHPLRFSEB GSGIYNDFA RVSSDHEAV NGILHFIDRV LLPPEALHWE PDDAPIPRRN VTAAGQFGY KIFSLIKVA GLLELREAS
BAA13377 1221 VGLRLRSED LLEQYATALL SGHPLRFSEB GSGIYNDFA RVSSDHEAV NGILHFIDRV LLPPEALHWE PDDAPIPRRN VTAAGQFGY KIFSLIKVA GLLELREAS

175SHARE 638 HTPTVFWPT DKALEALPPE QODPLFNQDN KDKLSYLYK HVIRDSKALA SDLERSASMK TLQGSSELVR STGSDIGEL FLNQGIRPI RHGLLFDVGV AYGIDLILN
BAB15793 415 HTPTVFWPT DKALEALPPE QODPLFNQDN KDKLSYLYK HVIRDSKALA SDLERSASMK TLQGSSELVR STGSDIGEL FLNQGIRPI RHGLLFDVGV AYGIDLILN
CAB61358 328 HTPTVFWPT DKALEALPPE QODPLFNQDN KDKLSYLYK HVIRDSKALA SDLERSASMK TLQGSSELVR STGSDIGEL FLNQGIRPI RHGLLFDVGV AYGIDLILN
AAF82398 120 HTPTVFWPT DKALEALPPE QODPLFNQDN KDKLSYLYK HVIRDSKALA SDLERSASMK TLQGSSELVR STGSDIGEL FLNQGIRPI RHGLLFDVGV AYGIDLILN
CAB61827 1758 HRPFMTLWPT DAAFRALPFD RQWLYHEDH RDKLAILLG HMIRNVEALA SDLNLGLPLR TMGTPLISFS STTRP-GEL MVGEDDARIV QRHLFFBGL AYGIDLILN
BAA13377 1401 HRPFMTLWPT DAAFRALPFD RQWLYHEDH RDKLAILLG HMIRNVEALA SDLNLGLPLR TMGTPLISFS STTRP-GEL MVGEDDARIV QRHLFFBGL AYGIDLILN

175SHARE 748 PTLGGRTDT TTFDIP-GE GSITPKP LKSKPKGVK K--LY-- --N-LPF R----- --RNVE-G QNLTUVIQT PRSHGYMP DQAEGGED
BAB15793 525 PTLGGRTDT TTFDAS-GE GSINTPSP RWSKPKGVK K--LY-- --N-LPF R----- --RNVE-G RERSLVIOI PRSHGYMP DQAEGGED
CAB61358 438 PTLGGRTDT TTFDAS-GE GSINTPSP RWSKPKGVK K--LY-- --N-LPF R----- --RNVE-G RERSLVIOI PRSHGYMP DQAEGGED
AAF82398 230 PTLGGRTDT TTFDAS-GE GSINTPSP RWSKPKGVK K--LY-- --N-LPF R----- --RNVE-G RERSLVIOI PRSHGYMP DQAEGGED
CAB61827 1867 PTLGGRTDT TTFDAS-GE GSINTPSP RWSKPKGVK K--LY-- --N-LPF R----- --RNVE-G RERSLVIOI PRSHGYMP DQAEGGED
BAA13377 1510 PTLGGRTDT TTFDAS-GE GSINTPSP RWSKPKGVK K--LY-- --N-LPF R----- --RNVE-G RERSLVIOI PRSHGYMP DQAEGGED

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BAB15793 609 PTLNNNGMR DLTFTMGOQL DTFGNQPA ELKHRRFGP DQPRSSSEH GQDDBSITGS GHLLEIGWT AASTDTFPAV FAVTEAASV HATKENNT VNLNBYSDG
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AAF82398 314 PTLNNNGMR DLTFTMGOQL DTFGNQPA ELKHRRFGP DQPRSSSEH GQDDBSITGS GHLLEIGWT AASTDTFPAV FAVTEAASV HATKENNT VNLNBYSDG
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AAF82398 424 ITTVVDK QNNG AKVA RSKQGTQVS SSKQYKGD GYSIELDP ADGWNGHE HATKMTGPG KHKEKSHY VGDGILN-EP EQPLDIRLQ INQGHPAS
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175SHARE 1052 ADLHFQDIT VGVFHLRSP QGYKLTFDKA REAANEAAAT MATYNQLSYA QKAKYHLSA GWLETGRVAY PTAPASQNG SGVVGIVDYG PRANKSEMD VFRYMKDN
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175SHARE 1162 ITKAGYVGD GFS-SGNLL QVLSMPSFLT NFLTEVLAFS KSSARGAPL KHLTDLISRG TLFVQNSGL GENETLSGRD IEHHLNVNV SPYNDLVNGT FLRMLGSQSL
BAB15793 938 ITKAGYVGD GFS-SGNLL QVLSMPSFLT NFLTEVLAFS KSSARGAPL KHLTDLISRG TLFVQNSGL GENETLSGRD IEHHLNVNV SPYNDLVNGT FLRMLGSQSL
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BAA13377 1950 ITKAGYVGD GFS-SGNLL QVLSMPSFLT NFLTEVLAFS KSSARGAPL KHLTDLISRG TLFVQNSGL GENETLSGRD IEHHLNVNV SPYNDLVNGT FLRMLGSQSL

175SHARE 1271 LITFS--QD QLHQ-ETRFV DGRSILQWDI IAANGILHI SEPLRAPPTA ATA---AHSG LGTIFCAV LVTGAIA--L AYSYFRIRK RTIG--FQHF DQKRTLSMWL
BAB15793 1047 LITAS--QD PLQPTETRFV DGRSILQWDI IAANGILHI SRPLKAPPAP VTL---THIG LGAGIFFAI LVTGAVA--L AYSYFRIRK RTIG--FQHF ESEEDINVA
CAB61358 924 LITAS--QD PLQPTETRFV DGRSILQWDI IAANGILHI SRPLKAPPAP VTL---THIG LGAGIFFAI LVTGAVA--L AYSYFRIRK RTIG--FQHF ESEEDINVA
AAF82398 742 LITAS--QD PLQPTETRFV DGRSILQWDI IAANGILHI SRPLKAPPAP VTL---THIG LGAGIFFAI LVTGAVA--L AYSYFRIRK RTIG--FQHF ESEEDINVA
CAB61827 2056 IISDAGPENS SWAPVAGTV VVSIIWMDI MAFNGIITHAL ASPLLAPPQ QAVLAPEAP VAAGV--GAV LAAGALLGLV AGALYLRAG KPMGPFSAF QAEDDADDF
BAA13377 2166 IISDAGPENS SWAPVAGTV VVSIIWMDI MAFNGIITHAL ASPLLAPPQ QAVLAPEAP VAAGV--GAV LAAGALLGLV AGALYLRAG KPMGPFSAF QAEDDADDF

175SHARE 1370 LASSSP-RIS QTLQRPQR HOSPPVTPS QTLNRIWRT ATLMHGCPD MRSQQAATV VFR
BAB15793 1147 LQKQPENIS NFLY-ESTTS APFPPSYDP TDSER--- --QLEGNDF LRIL
CAB61358 1024 LQKQPENIS NFLY-ESTTS APFPPSYDP TDSER--- --QLEGNDF LRIL
AAF82398 852 LQKQPENIS NFLY-ESTTS APFPPSYDP TDSER--- --QLEGNDF LRIL
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Figure 29

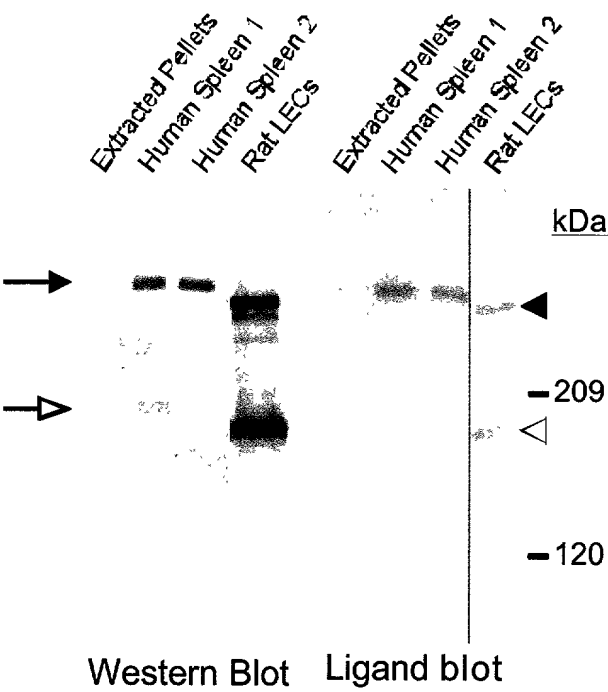


Figure 3 0

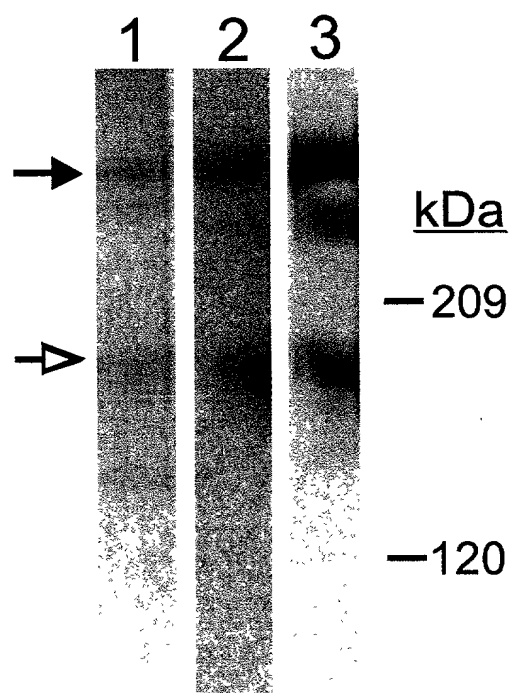


Figure 31

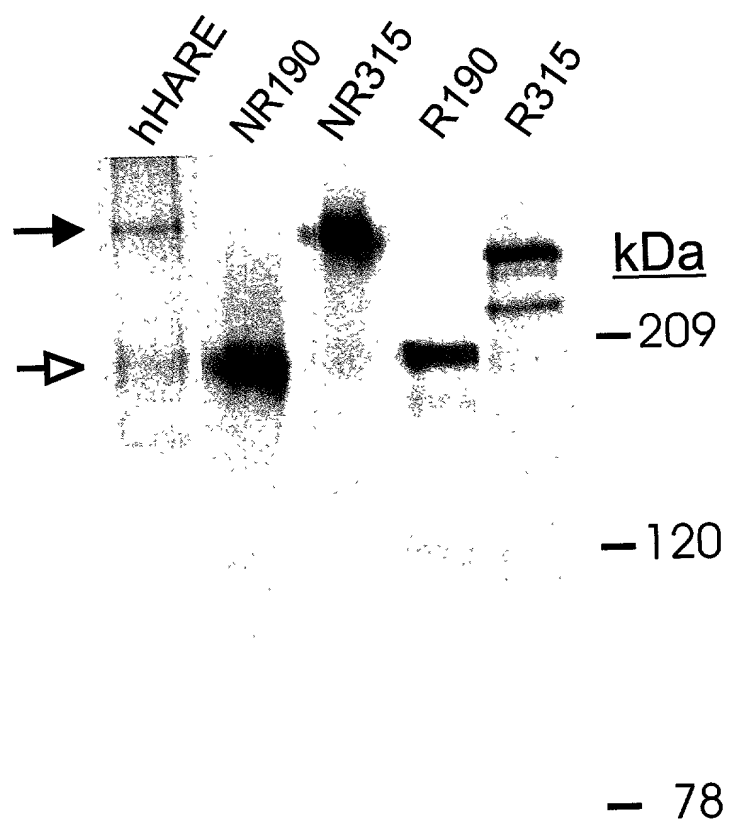


Figure 3 2

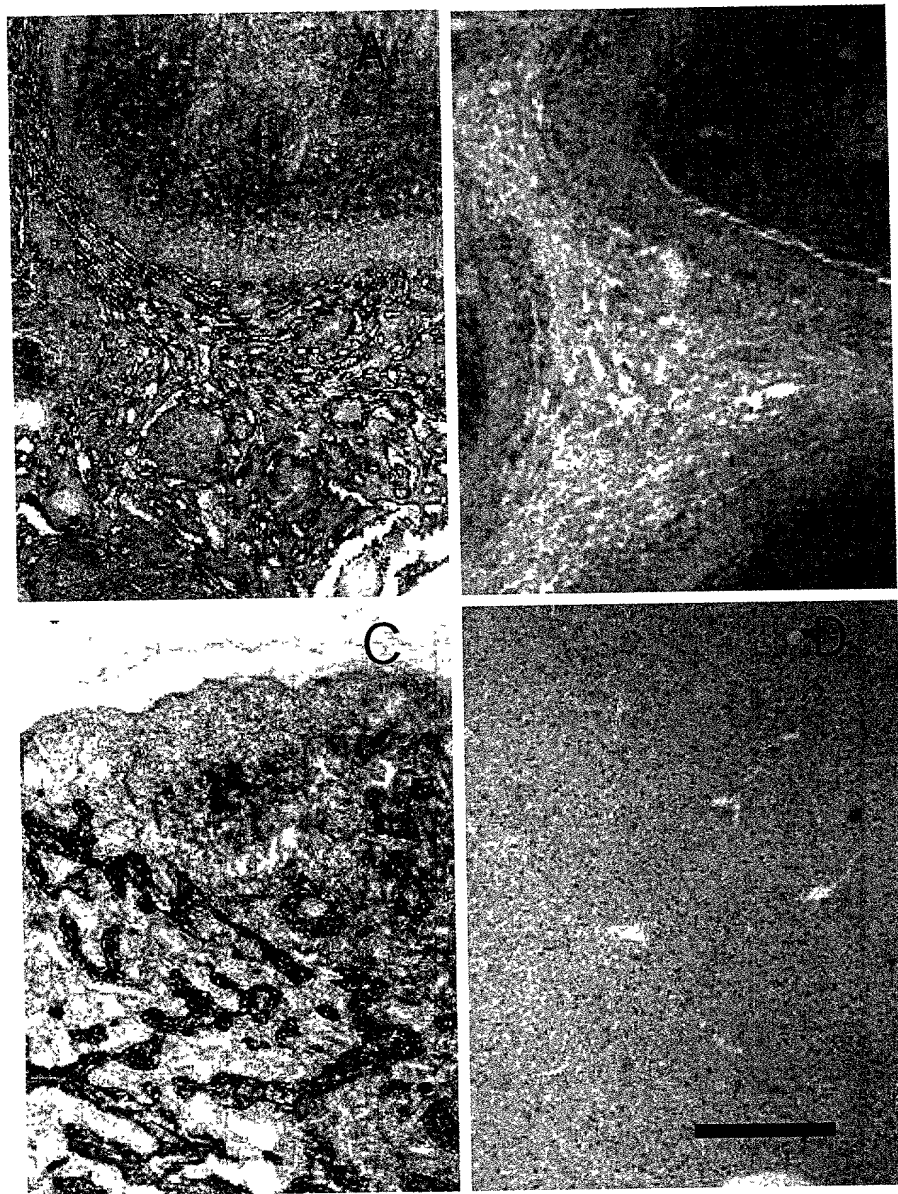


Figure 33

1 ATTCATATATATCGGCGAATGCAATTGAGGCTGCCGATGCTTACAGTGTGTGCTCCAAACAAACATGCCATCGAGAATTACATCAGGGAGAAGAAAGCTCTGTCTCTAGAGGAGGAC
1 I Q Y N L A N A T E A D A Y T V F A P N N A I E N Y I R E K K V L S L E E D

121 GTCTCCGGATCATGTGGTCTCGGAGGAAATCTCTGAAGATGACCTGCACATGGCATCTGTGAGCAGCATGTGGGTTTCTCTATTTCCTAGCTTCTTCTCCATATGAC
41 V L R Y Y H V V L E E K L L K N D L H N G M M H R E T M L G F S Y F L S F F L H N D

241 CAGCTCTATGTAATGAGGCTCCAATAACATCAACCACTGATGACCTGATAGGAGGTGATCTCATGGCTTGGGAAATTTCTCGAAATTCAGAAACAGCATGTGATATATGACACT
81 Q L Y V N E A P I N Y T N V A T D K G V I H G L G K V L G L E I Q K N R C D N N D T

361 ACTATTATCAGGAGAGATGTAGACCTCTCTCCAGCTGACCTGCCCATTCGGAATCTCTCTAGGTATGAGAAGAGGAGATGCATCTATACCTCTTATTTTCATGGGAAGACGA
121 T I I R R G R C R T C T S C E L L T C F F A G T K S L G N E K R R C I Y T S Y F M G R R

481 ACCCTGTTTATTGGGTCCGACGCAAAATGTGTGAGAACCGCTATTACGAGAAATGCTGTGCGGGCTCTTTGGCCCCAATGCCAGCCCTGTCCAGGAATGCCAGAAATGCTGCTTT
161 T L F I G C Q P K C V R T V I T R E C C A G F F G P Q C C Q C P C P G N A Q C N V C F

601 GGTAAATGGCATCTGTTGGATGGAGTGAATGGCAGAGTGTGTGAGTGTGGGGAGGGCTTCAGCGCCAGAGCTTCAGAGACTGCACCGAGGCGAAGTACGGGCATCCCTGTGACCAA
201 G N G I C L D G V N G T G V C E G E G F S G T A C E T C T E G K Y G I H C D Q

721 GCATGTTCTGTGTCCGAGGATGCACCAAGAGACCTTGGGAGATGGCTCTGTGACTGATGTGTGCTGGCGAGGATGATGTGACCAATGCAACACAGAGCAACTGCAA
241 A C S C V H G R C N Q G P L G D G S C D C D V G N R G V H C D N A T T E D N C N

841 GGGACATGCCATACCAGCGCAACTGCCCTCACCACTCAGATGGTACAGCTTCATGCAAGTGTGCAGCAGGATTCACAGGAAACGGGACCTTCACAGCAATCAATGCCCTGTGAGATC
281 G T C H T S A N C L T N S D G T A S C K C A A G F Q G N G T I C T A I N A C E I

961 AGCAATGGAGTGTCTCTGCCAAGGCTGACTGAAGAGAACCCAGGAGGCGAGTGTGCACGTGCAAGAGCAGGCTACCGGGTATGGCATCTGTGTGCTGGAAATCAACCGGCTGT
321 S N G G C S A K A D K R T P G R R V T C K A G Y C T G D G I V G I H C D Q

1081 TTGAGAACCAATGGTGGCTGTGACAGAAATGCGGAGTGCCACAGCAGGACCCAAACAGGCTGCCCTGTAAGCTTTGGCCAGCATACCTGAGAGATGGAAGAGTGTGCACACTCATCAAT
361 L E N H G G C D K N A E C T Q T G P N Q A A C N C L P A Y T G D G K V C T L I N

1201 GTCTGTCTAACTAAATGGCGGCTGTAGTGAATTGCCATCTGCAACCACTGCGGCAAGTAGAAGGACTTGTACTTGCAGGCAAACTACATTGGAGATGGATTTACCTGCCCGGG
401 V C L T K K G G C S E F A I C N H T G Q V E R T C T C K P N Y I G D G F T A C T R K I G

1321 AGCATTTTATCAGGAGCTTCCCAAGAACCCGAAATCTCCAGTATTTCTCCAGTGTGAGGAGATTCCTGTAAAGATCTGTGTGCGGCCAGGCCCTTCACTGTTTGTACCTTTATCT
441 S I Y Q E L P K N P K T S Q Y F F Q L Q E H F V K D L L V G P G P P T V F A P L S

1441 GCAGCTTTGATGAGGAAGCTCGGCTTAAAGCTGGGACAAATACGGTTTAAATGCCCAAGGTTCTTCGTACCATGTGTGTGCTGCCACAGCTGCTTGGAAATCCGGAATGTATC
481 A A F D E A R V K D W K I Y G L M P Q V L R Y H V Y V A C H Q L L L E N K L I

1561 TCAAAATGCTATCTCCCTCAAGGAGGACCAATGATCATCTCGCTCTCTCAGAGCAGGCTGTATAAACAAATAGGCTAAGATCATATCCAGTATATCATAGTCAATGGGATGTGT
521 S N A T S L Q G E P I A V I T I S V S Q S T V Y I N N K A I I S S T I S T N G I V

1681 CATATCATAGACAAATGTCTATCTCCCAAAATTTGCTTATCACTCCCAAGACAACTTGGAGAATTCTGCAAAATCTTACGACTTTGGCAACAAACATGGCTCATCAAAATTAGC
561 H I I D K L S P K N L L I T P K D N S G R I L Q N L T T L A T N N G Y I K F S

1801 AACTTAATACAGGATCAGGTTGTCTGAGTGTCTACCGATCCCATCACCCAGCTCATCTTCTGGCCCAACGACCAAGCCCTCCATGCCCTACTGCTGAACACAGGAGCTTC
601 N L I I Q D S G L L S V I T D P I H T P V T L F W P T D Q A C A L H A L P A E Q Q D F

1921 CTGTTCAACCAAGAACACAGGACCACTGAGGAGTATTGAAGTTTTCATGTGATACAGGATGCCAAGTTTTCATGTGATCTTCCCACTATCCATGCCCTGGAAACCTGCAAGGTT
641 L F N Q D N K D K L K E Y L K F H V I R D A K V L A V D L P T S T A W K I L Q G

2041 TTAGAGCTGAGTGTGAATGTGAGCTGGCAGGACATCGTGACCTCTTGTGAATGGCCAACTCGAGAATTGTGAGCGGGAGCTCTGTTTGACCTGGGTGTGGCTTACGGCAT
681 S E L S V K I C G A G R I G D L F L N G Q T C R I V Q R E L F L F D L G V A Y G I

2161 GACTGTCTCTGATTGATCCCACTCGGGGGCGCTGTGACACCTTTACTACTTTCATGCTCTGGGGAGTGTGGAGCTGTGTCAATCTCCAGCTGCCCAAGTGTGATGAACCA
721 D C L L I I D P T L G R C D T F T T T F D A S G E C G S C V N T P S C P R N S K P

2281 AAGGTGTGAACAGAGATCTCTCAACCTCGCTCTCAAGAGGAACTGGAAGGCTCGGGAGCGCTGCAGCTGATGATACAGATCCCAGGTGCTGCAAGCTTCTCGGGCG
761 K G V K Q K C L Y N L P F K R N A C T L E G C R E R S T G V I Q I P R C K G Y G R A

2401 GACTGTGAGGCTGCCCTGGAGGACGATGCCCGGTGAATAACACGGGGTGTCTGCTGTATGATCATCTGGCCACCGGAGAGTGAATGCAACACCGGCTTCAATGGAGCGGGGTGT
801 D Q A C P G G P D A P C N N R G V C L D Q Y S A T G E C K C N T G F N G T A C

2521 GAGATGTCTGGCCGGGAGATTTGGCGCTGATTGTCTGCCCTGTGGCTGCTCAGACCAAGGACAGTGCATGATGGCATCCGGGCTCGGGCAGTGCCTCTGTGAACGGGGTGGACA
841 E M C W G R F G P D C L F C G S D H G Q C D D G I T G S G Q C L C E T G N T

2641 GGCCCCCTGTGTGACACTCAGCAGCTTTGCCCTGAGTGTGACGCTCTTGTCTGATCTGACCTGCAATGAGGAGAACCAAGCTGTGAGTGTAACTGATTGAAGGTGACGGA
881 G P S C D T Q A V L P A V C T P P C S A H A T C K E N N T C E C N L D Y E G D G

2761 ATCAGTCCAGCTGTGGATTTCTGCAACAGGACCGGGGCTGTGCAAGGTTGGCCAGATGCTCCAGAAAGGACAGAGGTCTCTGCACTGCCAAGGAGATCAAGAGGGAC
921 I T C T V D F C K Q D N G G C A K A V A K C S Q K G T K V S C S C Q K G Y K G D

2881 GGGCAGCTGCAACAGAGATGACCCCTGTGAGACGGCTTAAAGGGGGTGTCAAGGACCACTGTAAGTACAGGCCCCGGGCAAGCAAGTGTGAGTGTAAAGATCATAT
961 G H S C T C E I D P C A D G L N G G C H E H A T C K M T G P G K H K C E K S H Y

3001 GTCCGAGATGGGCTGAATCTGTAGCGGGAGCTGCCATGTGACCCTGTACAGGACAAATGGCAGTGCATGACAGCGCCAAATGTGTGACCTCCACTTCCAGGATACCATCTGT
1001 V G D G L N C E P Q I F I D R C L Q D N G Q C H A D A K C V C Q D D G I T G S G Q C L C E T G N T

3121 GGGGTGTTCATCTACGCTTCCACCTGGGCGAGTAAAGCTGACCTTTGACAAACAGGAGGCTGTGCAACGAGCTGCAAGTACGCACTGCAACCTCAACAGCTCTCTATGGCCAG
1041 G V F P H L R S P L G Q Y K L T F D K A R I E A C A N E A A T M A T Y N Q L S Y A Q

3241 AAGCGCAAGTACCACTGTGCTCAGCAGCTGGCTGGAAGACGGGGCGGTTGCCATACCCACAGCTTCGCTCCAGAACTGTGGCTCTGTTGGGATGTGGAATGGAATGCAATGACCT
1081 K A K Y H L C S A G G N L E T G R V A Y P T A F S N C G S G V Y G I V D Y G P

3361 AGACCCCAAGAGTGAATGTGGGATCTTCTGCTATCGGATGAAGATGTGAATGCACCTGCAAGGTGGCTGTGAGGAGATGCTCTCATGAGTGGGAACTGCTGCAGGTC
1121 R P N K S E M W D V F C Y R M K D V N C T C K A V Y V G D G F S C S G N L L Q V

3481 CTGATGTCTCTCCCTCACTCAAACTTCTGACGGAAGTGTGGCTTATTCACACAGCTCAGCTCGAGGCGGTGATTTAGAACCTGACGTGACCTGTGCAATCGGCGGACCTCT
1161 L M S F P S L T N F L T E V L A Y S N S S A A R G R A F L E H L T D A C T S I R G C G T L

3601 TTGTGCCACAGACGTGGGCTGGGGAGATGAGACCTTGTGTGGCGGGACCTGAGGACCACTCGCAATGTGTCAGATGTTTTCATCAATGACCTTGTCAATGGGCAACCTG
1201 F V P Q N S G L G E N E T L S G R D I E H H L A N V S M F F Y N D L V N G T L

3721 CAACAGGCTGGGAAGCAGCTGTCTATCTGACGAGGACCACTCCAACTCGGAGACAGCTTGTGTGATGGAAGGCAATTCGATGGGATCTTGTGCTCCATGGG
1241 Q T R L S G S K L L I T A S C Q D P L C P T E R T F V D G R A I L Q W D I F A S N G

3841 ATCATTATGTCAATTCAGGCTTTTAAAGACACCCCTGCCCCGTGACCTTGACCCACATGGCTTGGGAGCAGGATCTTCTTGTGATCATCTGCTGAGTGGGGCTGTGCTCTG
1281 I H H Y I S R P L K A P P A P V T L T H T G L G A G A C K C Y I F F A I I L V T G A V A L

3961 GCTGCTTACTCTCTATCTCGGATAAACCGGAGCAATCGCTTTCAGCATTTTGTGATCGAAGAGCAATTAATGTTGACCTTGGCAGCAGCAGCTGAGAATCTCGAAGCCC
1321 A A Y S Y F R I N R R T I G F Q H F E S E E D I N V A I L G K Q Q P E N I S N P

4081 TTGATGAGAGCAAACTCAGCTCCCCAGCACTCTCTACGACCCCTTCAGGATCTGGAAGACCGGACCTTGAAGGCAATGACCCCTGAGGACATGTGAGGCGCTGGAAGGGAG
1361 L Y E S T T S A P P E P S Y D P F T D S E A E R Q L E G N D P L R T L S (1394aa)

4201 ATCGGACGCTCATCTCACTGCCACTGGGCCATCAACTGTGAATTTCTCAGCAGCAGTGGCTTTTAGGAACGTAAAGTCTTTAGGCACTCAGAAGCCATACCTCATCTCTGCTGTGAT
432

Figure 35

hHARE 1 IOYNLANATEAADAYTVFAP NNAIENYIREKKVLSLEED VLRHVVLBEKLLKNDLHNG MHRETMLGFSYFLSFFLLHND QLYVNEAPINYNVATDKGV
rHARE 23 IHYNLASATESADAYTVFVP NNEAIENYIREKATSLKED ILRYHVVLGEKLLKNDLHNG MHRETMLGFSYLLAFLRLND QLYVNEAPINYNVATDKGV

hHARE 101 IHGLGKVLBIQKNN DNDTA TIIRGR RT ISSELT PFGT KSLGNEKRR IYTSYFMGRR TLFIG QPK VRTVITRE C AGFFPGQCPQCPGNAQNVCF
rHARE 123 IHGLEKVLBIQKNN DNDTA IIVRGE GK SQAP PLET IIVRGE GK SQAP PLET KPL-RETRK IYTSYFMGR SVFIG QPK VRTITRA W LASLAHNAKPAPEVKMCAL

hHARE 201 GNGICLDGVNGTGV E GEG FSGTA ET TEGKYGIH DQ A S VHG R NOGPLDGS D DVGWRGVH DNATETDN N G HTSAN LTNSDGTAS K
rHARE 222 GTASVWDGVNGTGV O GLG FNGTA ET TEGKYGIH DQ A S VHG R SOGPLDGS D DVGWRGVK DMEITTDN K G HTSAN LLDPDGKAS K

hHARE 301 AAGFOGNGTI TAINA EI SNGG ISAKAD KRTPPGRV T KAGYTG DGIV LEINP LENHGG DNAB TOTGPNQ AAN LPAYTGDGKV TLIN
rHARE 322 AAGFRGNGTV TAINA ET SNGG STKAD KRTPGNRV V KAGYTG DGIV LEINP LENHGG DRNAE TOTGPNQ AVN LPAYTGDGKV SLIN

hHARE 401 VLTNNGG SEFAI NNN Q VERT T KENYIGDGT RG SIYQELPKNPKTSQYFFOLQ EHFVKDLVGPPTVFAPLS AAFDEEARVKDWDKYGLMPQ
rHARE 422 VLTNNGG SPFAF NNT Q DQRI T KPDYTG DGIV RG SIYGELPKNPSTSQYFFOLQ EHAURELAGPGPTVFAPLS SSFNHEPRKIDWDQOGLMSQ

hHARE 501 VLRHVVA HOLLLENKLI SNATSLQGEPIVTSVSQSTV YINNAKATISSDIISTNGIV HIIDKLLSPKNLLITPKDMS GRILQNEATLATNNGYIKFS
rHARE 522 VLRHVVG QOLLLENKVT TSATTLQGEFVSISVSQDTV FINNEAKVLSSDIISTNGVI HVIDKLLSPKNLLITPKDAL GRVLQNEATLATNNGYIKFS

hHARE 601 NLIQDSGLLSVITDPIHTPV TLFWPTDQALHALPAEQQDF LFNQDNKDKLKEYLKFHVIR DAKVLAVDLPTSTAWKTLQG SELSVK GAGRDIGDLFLNG
rHARE 622 KLIQDSGLLSVITDSIHTPV TVFWPTDKALEALPPEQQDF LFNQDNKDKLKEYLKFHVIR DSKALASDLPRSASWKTLQG SELSVR GTGSDIGELFLNE

hHARE 701 QTRIVQRELLFDLGAVYGI D LLLIDPTLGGRTDTFTTFD ASGE GS VNTPS PRWSKP KGVKQK LYN-LPFKRNLEG RER SLVITQIPR KGYFG
rHARE 722 QMRFIHRGLLFDVGAVYGI D LLMNPTLGGRTDTFTTFD IPGE GS IFTPK PLKSKP KGVKKR IYNPLPFRNVEG QNL TVVITQTPR KHYFPM

hHARE 800 RDQA PGGPDAP NNRGV LDQYSATGE KNTGFNGHA EM WPGRFGPD LPCG SD HGQ DDGITGSGQL ETGW TGPS DTQAVLPV TTPS
rHARE 822 PDQA PGGPDTP NNRGM RDLYTPMGQL HTGFNGHA EL WHGRFGPD QPRS SE HGQ DEGITGSGEL ETGW TAAS DTPAVFAV TPA S

hHARE 900 AHAT KENNT E NLDYEGD GIT TVVDF KQNGG AKV AR SQKGTQVS S KGYKG DGHS TEIDP ADGLNGGH EHAT KMTGPGKHK E KSH
rHARE 922 VHAT TENNT V NLNYEGD GIT TVVDF KQNGG AKV AK SQKGTQVS S KGYKG DGYS IEIDP ADGVNGGH EHAT RMTGPGKHK E KSH

hHAR 1000 YVGDGLN EPEQLPIDR LQ DNGQ HADAK VDLHFQDIT VGVFHLRSPGLGQYKLTFDKA REA ANEAATMATYNQLSYA QKAKYHL SAGWLETGRVAY
rHARE 1022 YVGDGVD EPEQLPLDR LQ DNGQ HPDAS ADLYFQDIT VGVFHLRSPGLGQYKLTFDKA KEA AKEAATMATYNQLSYA QKAKYHL SAGWLESGRVAY

hHARE 1100 PTAFASQN GSGVVGIVDYG PRPKSEMMWDF YRMKDVN KAGYVGDGFS SGNLLQ VLMSFPSTNFLTVEVLAYSN SSARGRAFLHLTDLDSIRGT
rHARE 1122 PTTVASQK GANVVGIVDYG SRANKSEMMWDF YRMKDVN KAGYVGDGFS SGNLLQ VLMSFPSTNFLTVEVLAFSK SSARGQAFLKHLTDLDSIRGT

hHARE 1200 LFVPQNSGLGENETLSGRDI EHLANVSMFFYNLDLVNGT LQTRLGSKLLITASQDPLQ LQTRFVDGRAILQWDIFASN GIITHVISRPLKAPPAPVTLT
rHARE 1222 LFVPQNSGLPGNKSLSGRDI EHLTNVNVVFFYNLDLVNGT LRTMLGSQLLITFSQDQLHQ -ETRFVDGRSILQWDIIAAN GILHI ISEPLRAPPTAATAA

hHARE 1300 HTGLGAGIFFAILIWTGAVA LAASYFRINRRITICFOHFE SEED INVAALGKQOPENISN PTESTAPPEPSDPPTD SEERQLEGNDDPLRTL
rHARE 1321 HSGLGTGIFCAVLTGAVA LAASYFRIKQRTGFORFD QKRTLMWSLLASSSPRISQT LCHRPQRHHPQSPVAPSQT LENRIWRATLWGHCGGPDMR

rHARE 1421 SQATTVTVPR

Figure 36

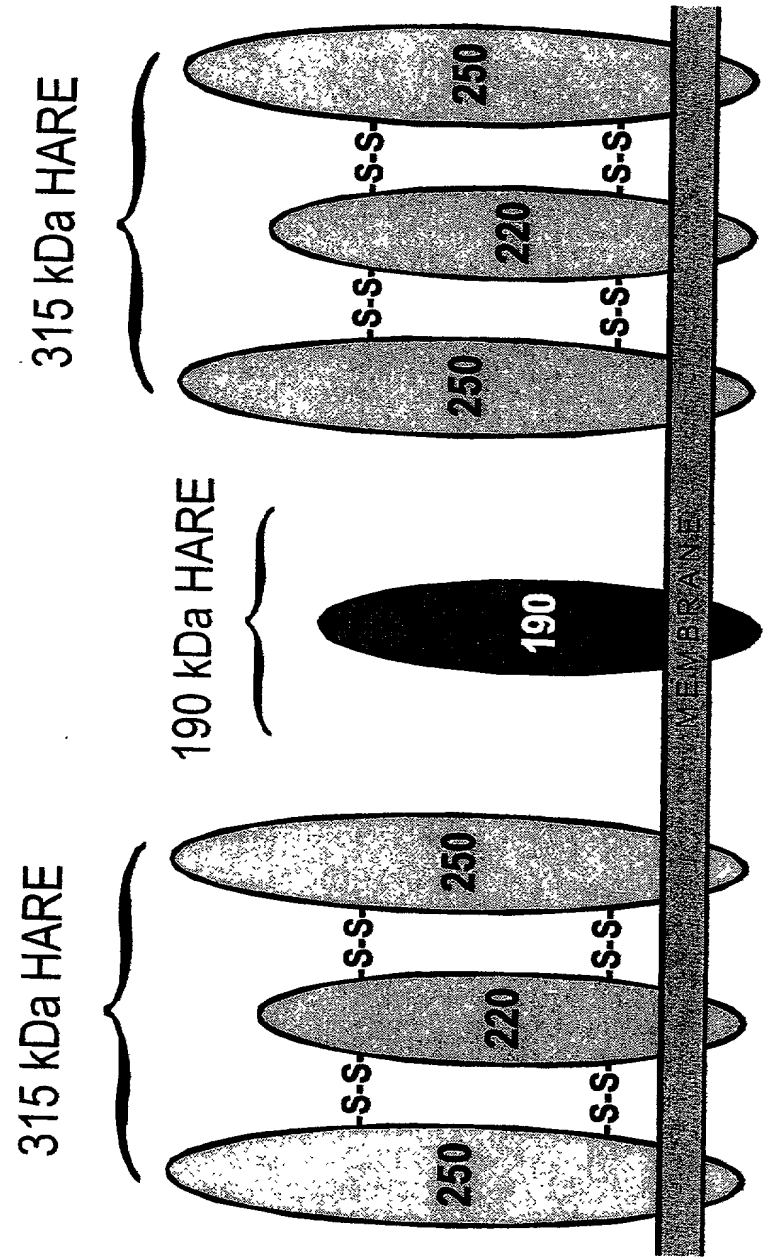


Figure 37

Amplification of the 1394 amino acid HARE
Open Reading Frame from a human lymph
node cDNA Library

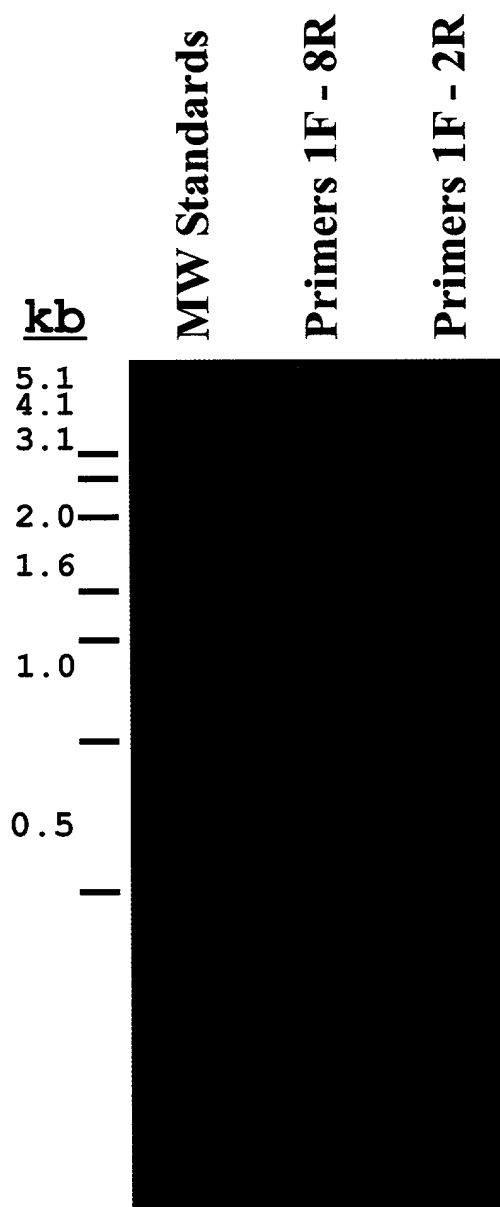


Figure 38

Schematic Organization of the Human HARE Gene on Chromosome 12
(encoding 1357 of the 1394 amino acids disclosed here)

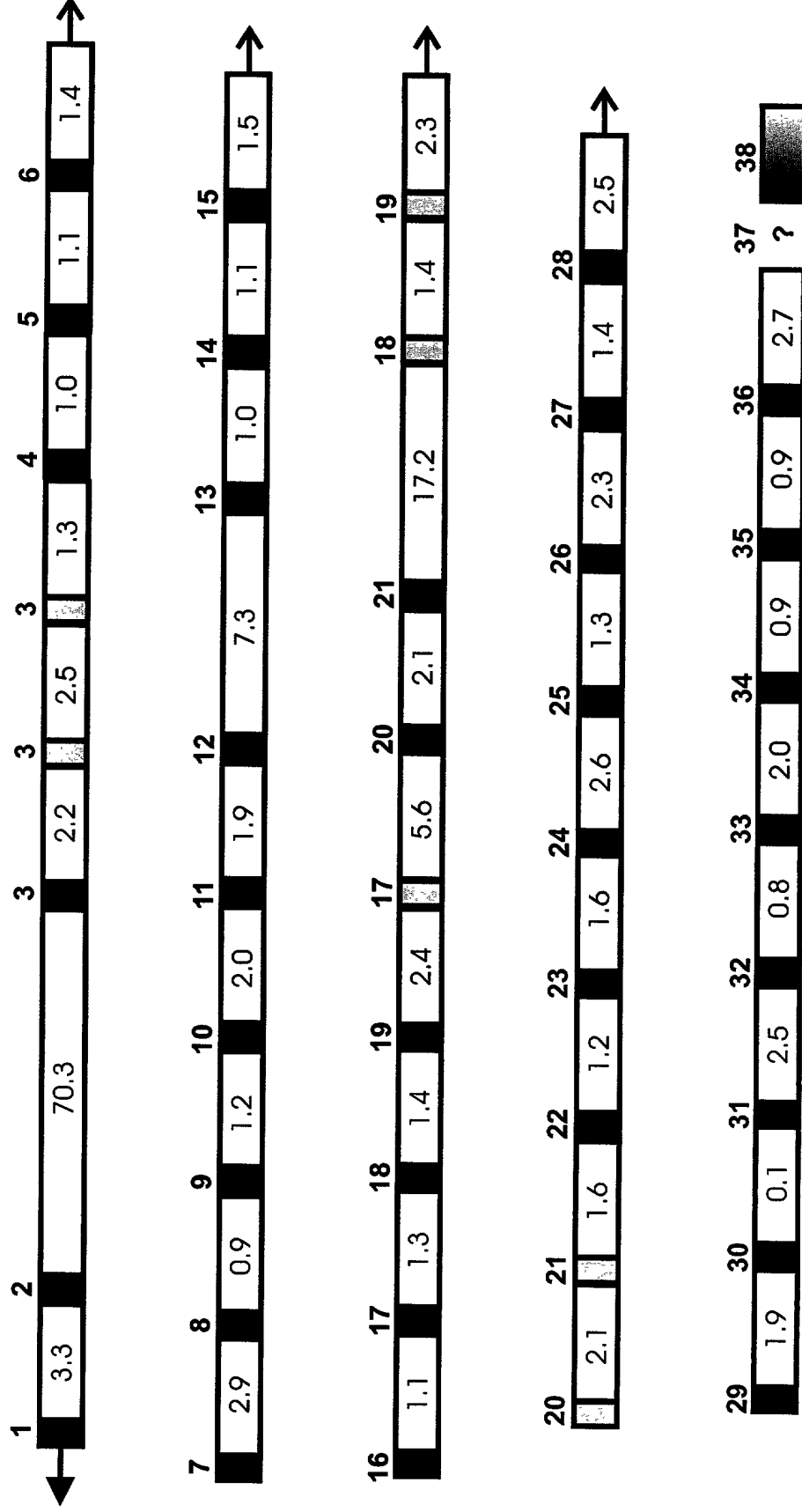


Figure 3 9

